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5.1.6 Compugen Ltd.	Search time 3903 Seconds (without alignments) 9633.111 Million cell undates/sec	taactcagccggcggttaa 1035		residues	ers: 65645750					results predicted by chance to have a 1 to the score of the result being printed, of the total score distribution.		Description	CF558062 1115033F0 CF565551 1115101B0	CF565552 1115101B0 CF558063 1115033F0	CL656958 PK10128a CF561913 1115069D0	CES63205 IIIS082A0 CL657503 PRIO1294 CF643306 111608380	BE423296 WHEOOG3 E AF075794 AF075794	CF915072 B0973F11- CF915603 B0982E05-	CF544559 Hd mx17 6 CF326686 Hd mx24 0 CN82461 O3 enlhn	BZ561117 pacs2-164 BZ570213 msh2_1236	BZ554003 pacs1-60 BZ562758 pacs2-164 BZ570029 msh2 1132	CR337045 Medi <u>c</u> ago BZ575847 msh2 4654 CK991504 EST0Ō56 E
GenCore version S Copyright (c) 1993 - 2005 (	OM nucleic - nucleic search, using sw model Run on: January 19, 2005, 13:25:53; £ 9(6)	Title: US-09-913-772-1 Perfect score: 1035 Sequence: 1 atgaaagcaattttcgtact	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 32822875 seqs, 18219865908 res	Total number of hits satisfying chosen parameters:	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	S	2: qD est2:* 3: qD_htc:* 4: gD_est3:* 5: qD_est4:* 6: qD_est5:* 7: qD_est6:* 8: qD_qss1:*	: gb_gss2:* s the number of er than or equa ved by analysis	SUMMARIES	Result Query No. Score Match Length DB ID	1 461.6 44.6 671 7 2 454.8 43.9 628 7	426 41.2 639 7 396 38.3 591 7	6 274 26.5 422 7	219 21.2 730 9	10 159 15.4 603 2 11 134.2 13.0 655 8	61.4 5.9 601 7	61.4 5.9 736 61.4 5.9 763 61.4 5.9 860	56.6 5.5 1047 8 54.8 5.3 748 8	19 54.8 5.3 1030 8 20 53.4 5.2 773 8 21 53.2 5.1 912 8	22 51.6 5.0 134 9 CR337045 c 23 51.6 5.0 1772 8 BZ575847 c 24 49.6 4.8 600 7 CK991504

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## ALIGNMENTS

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flask with 98 % nitrogen, 35 CO2 gas mixture for 1 hour prior to harvesting for RNA isolation (as per Quinn UN Barraco P. Eriksson M, Merchant S. Quinn et al. (2000) JBC 275:6080-6089; CC-1650 cells grown to mid-log phase (3x10e6 cells/ml) in TAP medium in a shaking (150 rpm) illuminated (70 mole photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/ml, transferred to high light (11000 mol photon/m2/s) with shaking (150 rpm) and sampled at (0.5, 1,2,4,6,12 hrs), CC-1690 cells grown to mid-log phase in H8 medium in a shaking (150 rpm) and sampled at (0.5, 1,2,4,6,12 hrs), CC-1690 cells grown to mid-log phase in H8 medium in a shaking (150 rpm) and illuminated (70 mole photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/ml, transferred to high light (11000 mol photon/m2/s) with shaking (150 rpm) and sample, pooled and cDNA synthesized (see Shrager et al, Plant Physiol. 131, 401-408 for details). The cDNA was directionally cloned into lambda Zap II (Stratagene) in the ECORI (5.7) and Xhori (3) sites, pluescript II SK-
                            1:736-757) in a shaking illuminated incubator (same conditions as above). CC-1690 cells were grown to mid-log phase in TAP medium in a shaking illuminated incubator to a density of 8x106 cells/ml. The flask was transferred to a shaking platform (200 rpm) at room temperature (230) 12 micromole/m2/sec illumination and bubbled in a stoppered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmids were excised from the lambda ZAP clones by
superinfection with ExAssist (Stratagene) phage. The
library was normalized using method 4 described in Bonaldo
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(2002) Eukaryotic Cell,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 44.6%; Score 461.6; DB 7; Length 671; Best Local Similarity 83.3%; Pred. No. 5.7e-124; Matches 543; Conservative 0; Mismatches 94; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (1996) Genome Research 6: 791-806.
Merchant S.LaFontaine et al.
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(normalized), Lamuda zap 11.

/note="Vector: pBluescript II SK-; Site 1: EcoRI; Site_2: Knoi; Stress condition III library, constructed by Jeanette Quinn and Chinang-Wen Chang, combines cDNAs from Cc-1690 cells grown to mid-log phase in copper-free TAP medium (see Quinn and Merchant (1998) Methods in Enzymology, 2997:263-279) in a shaking (150 pm) illuminated (about 100 micromolog/m2/sec) incubator at 22 C (see Quinn and Merchant (1998) Methods in Enzymology, 2997:263-279); CC-1690 cells grown to mid-log phase in low Fee (1 micromolar Fe) TAP medium (see La Pontaine S, Quinn JM, Naxamoco SS, Page MD, Gohre V, Moseley JL, Kropat J, Merchant S.Lafontaine et al. (2002) Eukaryotic Cell, 1373-757) in a shaking illuminated incubator (same conditions as above): CC-1690 cells were grown to mid-log phase in TAP medium in a shaking illuminated incubator to a shaking platform (200 rpm) at room temperature (23C) 12 micromole/m2/sec illumination and bubbled in a stoppered flask with 98% nitrogen, 2% CO2 gas mixture for 1 hour prior to harvesting for RNA isolation (as per Quinn JM, Barraco P, Eriksson M, Merchant S. Quinn et al. (2000) JBC 275:680-6689); CC-1690 cells grown to mid-log phase (3x10e6 cells/m1) in TAP medium in a shaking (150 rpm) illuminated (70 mole photon/m2/sec) incubator at 27 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cells were diluted to 1x10e6 cells/ml, transferred to high light (11000 ml) photon/m2/s) with shaking (150 rpm) and sampled at (0.5, 1,2,4,6, 12 hrs); CC-1690 cells grown to mid-log phase in HS medium in a shaking (150 rpm)
                                                                                                                                                                                                                                                                                            CF565551 629 bp mRNA linear EST 23-SEP-2003 1115101B09.xl C. reinhardtii CC-1690 (mt+), Stress III (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA 3', mRNA
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Cells were diluted to 1x10e6 cells/ml, transferred to high
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 628)
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Merchant, S., Quinn, J. and Shrager, J.
Manalyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1115
Contact: Charles Hauser
DCMB Box 91000
Duke University
Duke University
Duke University
Fax: 919 613 8159
Fax: 919 613 8177
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/clone lib="C. reinhardtii CC-1690 (mt+), Stress III
(normalized), Lambda Zap II"
                                                                 791
                                                                                                   /organism="Chlamydomonas reinhardtii"
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/strain="CC-1690 wild type mt+ 21gr"
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Location/Qualifiers
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Chlamydomonas reinhardtii
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CF565551.1 GI:34991634
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/db xref="taxon:3055" (Jone 11b="C-1690 (mt+), Stress III (normalized), Lambda Zap II" (stress condition III library, constructed by Jeanete Quinn and Chiung wen chang, combines cDNAs from Jeanete Quinn and Merchant (1998) Methods in copper-free Tap medium (see Quinn and Merchant (1998) Methods in Enzymology, 2997:263-279); normalized about 100 micromole/m2/sec) incubator at 22 C (see Quinn and Merchant (1998) Methods in Bnzymology, 2997:263-279); CC-1690 cells grown to mid-log phase in low Fe (i micromolar Fe) TAP medium (see La Fontaine S, Quinn JM, Nakamoto SS, Page MD, Gohre V, Moselby Ju, Kropat J, Maxamoto SS, Page MD, Gohre V, Moselby Ju, Kropat J, I:736-757) in a shaking illuminated incubator (same conditions as above). CC-1690 cells were grown to mid-log phase in TAP medium in a shaking illuminated incubator (and density of 8x10e6 cells/m1. The flask was transferred to a shaking jlatform (200 pm) at room temperature (23C) 12 micromole/m2/sec illumination and bubbled in a stoppered flask with 98% nitrogen, 2% CC2 gas mixture for 1 hour prior to harvesting for RNA isolation (as per Quinn JM, Barraco P, Eriksson M, Merchant S. Quinn et al. (2000) JRC 275:6080-6089); CC-1690 cells grown to mid-log phase in HS medium in a shaking (150 rpm) illuminated (10 mole photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/m1, transferred to high light (11000 mol photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/m1, transferred to high light (11000 mol photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/m1, transferred to high light (11000 mol photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/m1, transferred to high light (11000 mol photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/m1, transferred to high light (11000 mol photon/m2/sec) second sample at (0.5, 1,2,4,6, 1,2 hrs); PolyA mRNA was directionally cloned an
Chlamydomonadaceae, Chlamydomonas.

1 (bases 1 to 639)
Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C.,
Merchant, S., Quinn, J. and Shrager, J.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Nicellular System for Analyzing Gene Function and Regulation in
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Chlamydomonas reinhardtii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 639.
Location/Qualifiers
                                                                                                                                                                                                               Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8175
Email: chauser@duke.edu
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light (11000 mol photon/m2/s) with shaking (150 rpm) and sampled at (0.5, 1,2,4,6, 12 hrs). PolyA mRNA was purified from each sample, pooled and cDNA synthesized (see Shrager et al, Plant Physiol. 131, 401-408 for details). The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK-plasmids were excised from the lambda ZAP clones by superinfection with ExAsist (Stratagene) phage. The library was normalized using method 4 described in Bonalde et al., (1996) Genome Research 6: 791-806."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAACATCGGCGAC 504
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Pred. No. 5.5e-122;
0; Mismatches 92;
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                                                  et al., (1996) Genome Research 6: 791-806."
                                                                                                                                          Length 639;
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CP558063 591 bp mRNA linear EST 23-SEP-2003 1115033F05.yl C. reinhardtii CC-1690 (mt+), Stress III (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA 5', mRNA
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Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
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Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C.,
Merchant, S., Quinn, J. and Shrager, J.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Punction and Regulation in
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                                                                                                          CCGGCACCGGAAGTACAGACCAAGCACTTCACTCTGAAGTCTGACGTTCTGTTCAACTTC
                                                                                                                                                                   AACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTG
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GGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCT
                        /mol_type="mRNA"
/strain="CC-1690 wild type mt+ 21gr"
/db xref="teaxon:3055"
/clone_lib="C. reinhardtii CC-1690 (mt+), Stress III
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Location/Qualifiers
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Unpublished (2003)
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DCMB Box 91000
Duke University
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Tel: 919 613 8159
Fax: 919 613 8177
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(Normalized), Lambda Zap II Sk-; Site I: ECORI; Site 2: Xhoī; Stress condition III library, constructed by Jennesd zondition III library, constructed by Jenneste Quinn and Chiung-Wen Chang, combines cDNAs from Jennette Quinn and Chiung-Wen Chang, combines cDNAs from C-1690 cells grown to mid-log phase in copper-free Tap medium (see Quinn and Merchant [1998) Methods in Enzymology, 2997:263-279); CC-1690 cells grown to mid-log phase in low Fe (1 micromolar Fe) Tap medium (see La Fontaine S, Quinn JM, Nakamoto SS, Page MD, Gohre V, Moseley JD, Kropat J, Maranoto SS, Page MD, Gohre V, Moseley JD, Kropat J, Maranoto SS, Page MD, Gohre V, Moseley JD, Kropat J, Maranoto SS, Page MD, Gohre V, Moseley JD, Kropat J, Maranoto SS, Page MD, Gohre V, Moseley JD, Kropat J, Maranoto SS, Page MD, Gohre V, Moseley JD, Kropat J, Maranoto SS, Page MD, Gohre V, Moseley JD, Kropat J, Maranoto SS, Page MD, Gohre V, Moseley JD, Kropat J, Maranoto SS, Page MD, Gohre V, Moseley JD, Kropat J, Maranoto SS, Page MD, Gohre V, Moseley JD, Kropat J, Maranoto SS, Page MD, Gohre V, Moseley JD, Kropat J, Maranoto SS, Page MD, Gohre V, Moseley JD, Kropat J, Maranoto SS, Page MD, Gohre V, Moseley JD, Kropat J, Maranoto SS, Page MD, Gohre V, Moseley JD, Kropat J, Maranoto SS, Page MD, Gohre V, Moseley JD, Kropat J, Maranoto SS, Page MD, Golre JD, Maranoto SP, Eriksson M, Merchant S. Quinn et al. (2000) JBC 275:6080-6089); CC-1690 cells grown to mid-log phase in HS medium in a shaking (150 rpm) and sampled at (0.5, 1,2,4,6, 12 hrs); CC-1690 cells grown to mid-log phase in HS medium in a shaking (150 rpm) and sampled at (0.5, 1,2,4,6, 12 hrs); CC-1690 cells grown as directionally cloned in Lambda Zap II (Straph and sample) potocon/m2/8ec) incubact at 27 C cells were diluted to lx10e6 cells/m1, transferred to high light (11000 mol photon/m2/8) with shaking (150 rpm) and sampled at (0.5, 1,2,4,6, 12 hrs); CC-1690 cells grown as directionally cloned into lambda Zap II (Straph was directionally Engele Stratagene) has superinfection with Exassista (Strata

ö 595 532 655 472 715 412 775 352 835 292 895 351 CCGACCGCATCGGTTCTGACGCTTACAACCAGGGTCTGTCCCGAGCGCCGTGCTCTG 536 GCATGCTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTG 591 GCATGCTGATCCTGGGTGTTTCTTACCGTTTGGGTCAGGGCGAAGCAGCCCCAGTAGTTG 596 CTCCGGCTCCGGCTCCGGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACG 531 CTCCGGCTCCAGCTCCGGCACCGGAAGTACAGACCAAGCACCTTCACTCTGAAGTCTGACG TGTACACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCTACA 411 TGTACAGCCAGCTGAGCAACCTGGATCCGAAGACGGTTCCGTAGTTGTTCTGGGTTACA CCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCG 836 TTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGCATGG 656 TICTGTICAACTICAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGC 471 Tricrigirica Actrica Acta Adea Actorida Adecesa Adeiro Aderica Gereciteda Trades Gaps .. Length 591; Indels tch 38.3%; Score 396; DB 7; L al Similarity 87.0%; Pred. No. 9.8e-105; 435; Conservative 0; Mismatches 65; Query Match Best Local Similarity 116 176 Matches 셤 g ò 셤 ò d ð g ò ò ઠ

232 955

896 GIGAAICCAACCCGGITACIGGCAACACCIGIGACAACGIGAAAGCICGCGCIGGACCIGA

291 rigingarraccidarcrocaaaggrarccceecaacaagarcrocecaceretaree

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/Glone lib=axonisuss.//clone lib axonisuss.//clone lib axonisuss.//clone lib axonisus condition III library, combines cDNas from Cc-1690 cells grown to mid-log phase in copper-free TAP medium (see Quinn and Merchant (1998) Methods in Enzymology, 2997:261-279)in a shaking(250 rpm) illuminated (about 100 micromole/m2/sec) incubator at 22 C (see Quinn and Merchant (1998) Methods in Enzymology, 2997:263-279); Cc-1690 cells grown to mid-log phase in low Fe (I micromolar Fe) TAP medium (see La Fontaine S, Quinn JM, Nakamoto SS, Page MD, Gohre V, Moseley JL, Kropat J, Merchant S.LaFontaine et al. (2002) Eukaryotic Cell, 1:736-757) in a shaking illuminated incubator to phase in TAP medium in a shaking illuminated incubator to a shaking platform (200 rpm) at room temperature (23C) l2 micromole/m2/sec illumination and bubbled in a stoppered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CF561913 422 bp mRNA linear EST 23-SEP-2003 1115069D01.x1 C. reinhardtii CC-1690 (mt+), Stress III (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA 3', mRNA
                                                                                                                                                                                                                                                                   971 CGGATCGTCGTCGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGG 1030
  CTGACGCTTACAACCAGGGTCTGTCCGAGCGCCGTGCTCAGTCTGTTGTTACCTGA 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales, Chlamydomonadaceae, Chlamydomonas.
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Merchant, S., Quinn, J. and Shrager, J.
Manalyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1115
Contact: Charles Hauser
DCMB Box 91000
                                                                                        TCTCCAAAGGTATCCCGGCAGACAAACATCTCCGCACGTGGTATGGGCGAACCCGG
                                                                                                                                                             TTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCTGATCGATTGCCTGGCTC
                                                                                                                                                                                                   407 TTACTGGCAACACCTGTGAACGTGAAACAGCGTGCTGCTGGACGATCGACTGCCTGGCTC
                                                                                                                                                                                                                                                                                                            347 CGGATCGTCGCGTAGAGATCGAAGTTAAAGGTATCAAAGACGTTGTAACTCAGCCGCAGG
                                                       TIGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGG
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|mol_type="mknA"
|strain="C2-1690 wild type mt+ 21gr"
|db_xref="taxon:3055"
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Location/Qualifiers
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Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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231 GCGAATCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAACAGCGTGCTGCACTGA 172
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Neodiplogasteridae; Pristionchus.
Srinivasa, J., Otto, G.W., Kahlow, U., Geisler, R., and Sommer, R.J. AppaDB: an AcedB database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db xref="taxon:54126"
/clone lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"
                                                    TCGATTGCCTGGCTCCGGATCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTG
                                                                                                      171 resacrecerecerecearcerecerasasarceaserraaserraaserras
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena,
sequenced at Vancouver, Canada.
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 0049701601371
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    .767
    /organism="Pristionchus"

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/strain="California"
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                                                                                                                                                          TAACTCAGCCGGCGGTTAA 1035
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CL656958
CL656958.1 GI:50137970
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Pristionchus pacificus
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Class: fosmid ends.
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g ò g 8 g 8 셤 Chlamydomonadaceae; Chlamydomonas.

(bases 1 to 438)

(cossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C.,
Merchant, S., Quinn, J. and Shrager, J.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Micellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1115
Unpublished (2003)
Contact: Charles Hauser
DCMB Box 91000
Duke University

AUTHORS

TITLE

COMMENT

organism="Chlamydomonas reinhardtii" /mol\_type="mRNA" /strain="CC-1690 wild type mt+ 21gr"

'db xref="taxon:3055"

High quality sequence stop: 438. Location/Qualifiers

FEATURES

Tel: 919 613 8159 Fax: 919 613 8177 Email: chauser@duke.edu Durham, NC 27708-1000

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flask with 98% nitrogen, 2% CO2 gas mixture for 1 hour prior to harvesting for RNA isolation (as per Quinn JW, Barraco P. Eriksson M, Merchant S. Quinn et al. (2000) JBC 275:6080-6089); CC-6500 cells grown to mid-log phase (3x10e6 cells/ml) in TAP medium in a shaking (150 rpm) illuminated (70 mole photon/m2/8ec) incubator at 27 C. Cells were diluted to 1x10e6 cells/ml, transferred to high light (11000 mol photon/m2/s) with shaking (150 rpm) and sampled at (0.5, 1,2,4,6, 12 hrs); CC-1590 cells grown to mid-log phase in HS medium in a shaking (150 rpm) illuminated (70 mole photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/ml, transferred to high light (11000 mol photon/m2/s) with shaking (150 rpm) and sampled at (0.5, 1,2,4,6, 12 hrs). PolyA mRNA was purified from each sample, pooled and cDNA synthesized (see Shrager et al, Plant Physiol. 131, 401-408 for details). The cDNA was directionally cloned into lambda Zap II (Stratagene) in the ECORI (5.) and XhORI (2.) sites, pluescript II SK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasmids were excised from the lambda ZAP clones by
superinfection with ExAssist (Stratagene) phage. The
library was normalized using method 4 described in Bonaldo
et al., (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGACCCGTAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 TCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACA 247
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/uncrealibeaconsisos.
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/note="Westor: pBluescript II SK-; Site 1: EcoRI; Site\_2:
/note="Westor: pBluescript II SK-; Site 1: EcoRI; Site\_2:
XhoI; Stress condition III library, combines cobMas from
Jeanette Quinn and Chiung-Wen Chang, combines cobMas from
CC-1690 cells grown to mid-log phase in copper-free TAP
medium (see Quinn and Merchant (1998) Methods in
Enzymology, 2997:262-279) in a shaking (250 rpm) illuminated
(about 100 micromole/m2/sec) incubator at 22 C (see Quinn
and Merchant (1998) Methods in Enzymology, 2997:63-279);
CC-1690 cells grown to mid-log phase in low Fe (I
micromolar Fe TAP medium (see La Fontaine S, Quinn JM,
Nakamoto SS, Page MD, Gohre V, Moseley JL, Kropat J,
Merchant S.Lasfontaine et al. (2002) Eukaryotic cell,
1:736-757) in a shaking illuminated incubator to
a phase in TAP medium in a shaking illuminated incubator to
a conditions as above). CC-1690 cells were grown to mid-log
phase in TAP medium in a shaking illuminated incubator to
a shaking platform (200 rpm) at room temperature (23C) 12
micromole/m2/sec illumination and bubbled in a stoppered
flack with one illumination and bubbled in a stoppered
flack with one illumination and bubbled in a stoppered

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349 CCAACAACATCGGTGACGCACACACCATCGGCACTCTTCCGGACAACGGCATGCTGAGTC 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGGCGTTTCCTAC 561
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            Matches 344; Conservative
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filask with 98% nitrogen, 2% CO2 gas mixture for 1 hour prior to harvesting for RNA isolation (as per Quinn by Barraco P, Erikeson M, Merchant S. Quinn et al. (2000) JBC 275.6080-6089), CC-1690 cells grown to mid-log phase (3x10e6 cells/ml) In TAP medium in a shaking (150 rpm) illuminated (70 mole photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/ml, transferred to high light (11000 mol photon/m2/s) with shaking (150 rpm) and sampled at (0.5, 1,2,4,6, 12 hrs); CC-1690 cells grown to mid-log phase in HS medium in a shaking (150 rpm) and simpled at (0.5, 1,2,4,6, 12 hrs); CC-1690 cells grown to light (11000 mol photon/m2/s) with shaking (150 rpm) and illuminated (70 mole photon/m2/sec) incubator at 27 C. Cells were diluted to 1x10e6 cells/ml, transferred to high light (11000 mol photon/m2/sec) incubator at 27 C. cells were diluted to 1x10e6 cells/ml, transferred to high sampled at (0.5, 1,24,6, 12 hrs). PolyA mRNA was purified from each sample, pooled and cDNA synthesized (see Shrager et al., Plant Physiol. 131, 401-408 for details). The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5) and XhoRI (3) sites pBluescript II SK-plant property control of the property of the part of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 superinfection with ExAssist (Stratagene) phage. The
library was normalized using method 4 described in Bonaldo
et al., (1996) Genome Research 6: 791-806."
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CF563205 438 bp mRNA linear EST 23-SEP-2003 1115082A08.x1 C. reinhardtii CC-1690 (mt+), Stress III (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA 3', mRNA

DEFINITION

Chlamydomonas reinhardtii Eukaryota, Viridiplantae; Chlorophyta, Chlorophyceae; Volvocales;

Chlamydomonas reinhardtii

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

GI:34989288

CF563205.1 sequence

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CF563206 323-SEP-2003 1115082A08.yl C. reinhardtii CC-1690 (mt+), Stress III (normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA 5', mRNA
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Chlamydomonas reinhardtii
Eukaryote; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 323)
Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C.,
Merchant, S., Quinn, J. and Shrager, J.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
                                                                                                                      GICTGAGAAACGTGCTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGG
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                                        CGTGAAAGCTCGCCCTGCCCTGATTGCCTGGCTCCGGATCGTCGTGGAGATCGA
      TTCCGCTGTTGTTCTGGGCTACACGGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCT
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/organism="Chlamydomonas reinhardtii"

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/strain="CC-1690 wild type mt+ 21gr"
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Location/Qualifiers
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Unpublished (2003)
Contact: Charles Hauser
DCMB Box 91000
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Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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   249
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                                                        GGCTTTGAAATGGGTTACGACTGGTTAGGTCGTATGCCGTACAAAGGCAGCGTTGAAAAC 146
                                                                                                                                                                        147 GGTGCATACAAAGCTCAGGGCGTTCAACTGACCGCTAAACTGGGTTACCCCAATCACTGAC 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCGCCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTT 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 730)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. Appabls an AcedB database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
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/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"
   GGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAAC
                                                                                                                   GGTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGAC
                                                                                                                                                                                                                                      GATCTGGACATCTACACCCGTCTGGGCGGCGATGGTTTGGCGCGCTGACTCCAAAGGCAAC
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Enail: raif. sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
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Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
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Pred. No. 9.4e-53;
0; Mismatches 40; Indels
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Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
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/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="california"
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Best Local Similarity 85.9%;
Matches 243; Conservative (
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CL657503
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GGTGTTT 438
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                                                                                                                                  FEATURES
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           a chaking platform (200 rpm) at room temperature (230) 12
micromols/m2/sec illumination and bubbled in a stoppered
flask with 98t nitrogen. 28 cO2 gas mixture for 1 hour
prior to harvesting for RNA isolation (as per Cuinn JM,
Barraco P, Eriksson M, Merchant S. Quinn et al. (2000) JBC
275:608-6089); CC-1690 cells grown to mid-10g phase
(3x1066 cells/m1) in TAP medium in a shaking (150 rpm)
illuminated (70 mole photon/m2/sec) incubator at 27 C.
Cells were diluted to 1x1066 cells/m1, transferred to high
light (11000 mol photon/m2/s) with shaking (150 rpm) and
sampled at (0.5, 1,2,4,6, 12 hrs); CC-1690 cells grown to
mid-10g phase in HS medium in a shaking (150 rpm)
illuminated (70 mole photon/m2/sec) incubator at 27 C.
Cells were diluted to 1x1066 cells/m1, transferred to high
illuminated (70 mole photon/m2/sec) incubator at 27 C.
Cells were diluted to 1x1066 cells/m1, transferred to high
light (11000 mol photon/m2/sec) incubator at 27 C.
Cells were diluted to 1x1066 cells/m1, transferred to high
sampled at (0.5, 1,2,4,6, 12 hrs). PolyA mRNA was purified
from each sample, pooled and cDNA synthesized (see Shrager
et al, Plant Physiol 131, 401-408 for details). The cDNA
was directionally cloned into lambda Zap II (Stratagene)
in the ECORI (5) and XhoRI (3) sites. pBluescript II SK-
plasmids were excised from the lambda Zap II (Stratagene)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bE442396
WHE0063_E04_I07ZS Wheat endosperm cDNA library Triticum aestivum cDNA clone WHE0063_E04_I07, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
8x10e6 cells/ml. The flask was transferred to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   863
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1 (bases 1 to 603)
Altenbach, S., Anderson, O.D., Chao, S., Galili, G., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAGGGTCTGTCCGAGCGCCGTGCTCTGTTGTTGATTACCTGATCTCCAAAGGTAT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACAC 923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 176; DB 7; Length 323;
Pred. No. 3.1e-40;
0; Mismatches 35; Indels
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84.9%;
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Matches 197; Conserva
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/db_xref="texnor:4565"
/clone="WHE0063 E04_107"
/tissue_type="Endosperm"
/dev_etage="texno.30 days post anthesis seed"
/dev_etage="texno.30 days post anthesis seed"
/lab_host="Texno.30 days post anthesis seed"
/lab_host="Texno.30 days post anthesis seed"
/lab_host="Texno.30 days to anthesis seed"
/lab_host="Texno.30 days to anthesis days anthesis seeds collected, endosperm isolated, and RNA_prepared by Susan Altenbach. Library constructed by Stratagene, Inc. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 AAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCTGGACA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 TCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGCTTCTA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             380 CCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCCAGTATTTGCTGGCGGCGTAG 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella typhimurium
Salmonella typhimurium
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wong R.M.-Y., Wong, K.K., Benson, N.R. and McClelland, M. Sample sequencing of a Salmonella typhimurium LT2 lambda library: comparison to the Escherichia coli Kl2 genome FEMS Microbiol. Lett. 173 (2), 411-423 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 TCTACACTCGTCTGGGTGGCATGGTATGGCGTGCAGACACTAAAATCCAA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 TGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGCTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 AAGCTCAGGGCGTTCAACTGACCGCTAAACTGGGTTACCCAATCACTGACGACCTGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Gaps
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 15.4%; Score 159; DB 2; Length 603; Best Local Similarity 77.9%; Pred. No. 3.6e-35; Matches 211; Conservative 0; Mismatches 45; Indels
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Class: shotgun.
                                                                                                                                                                                                                      organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440 AGIGGCTGTIACTCGTGACATCGCTACCCG 470
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                                                                                                                                                                                                                                                        /mol_type="mRNA"
/cultivar="Cheyenne"
                                                                                                                                                     Location/Qualifiers
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Sidney Kimmel Cancer Center
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Matches 104;
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
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B0973F11-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus
musculus cDNA clone NIA:B0973F11 IMAGE:30479302 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195 CGAAATGGGTTATGACTGGCTGGGCGTATGGCATATAAAGGCAGCGTTGACAACGGTGC 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
                                                                                                                                                                                                                                 /clone_lib="Salmonella typhimurium LT2, Lambda DASH II"
/note="Vector: Lambda DASH II; sequenced using Li-Cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 İGAAAACCAACİGGGGGGGGGGGTİTİGGİĞĞİİAĞCCAĞĞİİAAÇCCĞIATGİTĞĞCİİ
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National Institutes of Health
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0973 row: F column: 11
Seg primer: M13 Reverse
High quality sequence stop: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                               /organism="Salmonella typhimurium"
/mol_type="genomic DNA"
/strain="LT2"
                                                                                                                                                                                                                                                                                                                                                                                                          Score 134.2; DB 8;
Pred. No. 7.1e-28;
0; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
|srrain="C37BL/6J"
|db_xref="niaEST:B0973F11-5"
|db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 11 (9), 1553-1558 (2001)
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organism="Mus musculus"
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                                                                                                                                                                  /db_xref="taxon:602"
/clone="107-T3"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
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Best Local Similarity 72.7%;
Matches 194; Conservative
                                                                                                                                                                                                                                                                                                           sequencer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus
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TITLE
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MEDLINE
PUBMED
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LOCUS
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KEYWORDS
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FEATURES
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treated with T4 DNA polymerase, and purified by treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker Lib-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the CDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal1 and Not1 enzymes and cloned into Sal1/Not1 site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao."
                                                                                                                                                                                      /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: Sal1; Site_2: Not1; Mouse cDNA project by the Laboratory of Genefics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT)
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B0982E05-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus
musculus cDNA clone NIA:B0982E05 IMAGE:30480148 5', mRNA sequence.
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Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   814
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                                                                                                                     'clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        398
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Dirve, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0982 row: E column: 05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.9%; Score 61.4; DB 7; Length 601; 59.4%; Pred. No. 1.6e-06; ive 0; Mismatches 71; Indels (
/clone="NIA:B0973F11 IMAGE:30479302"
/dev stage="Unfertilized Egg"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 11 (9), 1553-1558 (2001)
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CK326686

Hd mx24 02F09 T7 Hypsibius dujardini mixed stage 5' capped (fraction 4') Hypsibius dujardini cDNs clone Hd mx24 02F09 5' similar to 652465 (652465) Protein F precursor (Fragment), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="whole body"

/dev stage="mixed (adult and juvenile)"

/clone_lib="Hyppiblius dujardini mixed stage (fraction 7)"

/clone_lib="Hyppiblius dujardini mixed stage (fraction 7)"

/note="vector: pSPORT; Site_1: Sal I (5'end); Site_2: Not

I (3'end); Tardigrades (alao know as water bears) are

small free living animals inhabiting marine, fresh water
and water film habitats. Hypsibius dujardini is a

may prepared from adults and juveniles and was constructed
by Jennifer Daub, University of Edinburgh."
                                                                                                                                                                   Tel: +44 131 650 6760

Fax: +44 131 670 5450

Email: mark.blaxteroed.ac.uk

The library was constructed from mixed stages of the tardigrade
Hypsibius dujardini maintained in lab culture. The original source
culture was obtained from Sciento (strain Z151). The library was
constructed by Jennifer Daub, University of Edinburgh. Sequencing
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417 CCCAGCGTCGTGCTGACGCTGTTAAGCAAGTCCTGGTCAAAGACGGTATTGCTCCTAACC 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Daub, J., Thomas, F., Aboobaker, A. and Blaxter, M.L.
A survey of genes expressed in the tardigrade Hypsibius dujardini
                                                                                                           Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        755 CCGCTGTTGTTCTGGGCTACACCGACCGCATCGGTTCCGAAGCTTACAACCAGCAGCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     875 AAAICICCGCTCGCGCAIGGGIGAAICCAACCCGGIIACIGGCAACACCIGIGA 929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                     Contact: Blaxter ML
Institute of Cell, Animal and Population Biology
University of Edinburgh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 61.4; DB 7;
Pred. No. 1.7e-06;
0; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Hypsibius dujardini"
/mol_type="mRNR"
/db_xref="taxon:232323"
/clone="Hd mx17 67B10"
/sex="parthenogenic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACKWARD: M13L
Plate: 67 row: B column: 10
Seq primer: 77 (TAATACGACTCACTATAGGG)
High quality sequence start: 6
High quality sequence stop: 533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Hypsibius dujardini
Eukaryota; Metazoa; Tardii
Hypsibiidae; Hypsibius.
1 (bases 1 to 763)
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CK326686.1 GI:40006296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.9%;
Best Local Similarity 59.4%;
Matches 104; Conservative
Jnpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                               FORWARD: M13R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                     fincte="Vector: pCMV-SPORT6 (Invitrogen); Site_1: Sal1; Site_2: Not1; Mouse cDNA project by the Laboratory of Genefics. National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgaun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treated with T4 DNA polymerase, and purified by ethanol-precipitation. The CDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/Chloroform, and separated from free linkers by Centricon 100. Then, the CDNAs were amplitied by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/Chloroform and Centricon 100. The CDNAs were digested with Sal1 and NotI enzymes and cloned into Sal1/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                    clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Tardigrada, Butardigrada, Apochela,
Eukaryota, Meypsibius.
Hypsibiidae, Hypsibius.
I (basea I to 73s) Aboobaker,A. and Blaxter,M.L.
Daub,J., Thomas,P., Aboobaker,A. and Blaxter,M.L.
A survey of genes expressed in the tardigrade Hypsibius dujardini
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was
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59.4%; Pred. No. 1.6e-06;
tive 0; Mismatches 71; Indels (
                                                                                                                                                                                                                                                                                  /clone="NIA:B098205 IMAGE:30480148"
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                                                                                                                                                                                                                                   xref="niaEST:B0982E05-5"
xref="taxon:10090"
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                                                                                                                                                   musculus"
Seq primer: M13 Reverse
High quality sequence stop: 601
POLYA=No.
                                                                                         Location/Qualifiers
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/strain="C57BL/6J"
                                                                                                                                                   organism="Mus"
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/note="Vector: pSPORTI; Site 1: Sal I (5'end); Site 2: Not all (3'end); Tardigrades (also know as water bears) are amal free living animals inhabiting marine, fresh water and water film habitats. Hypsibius dujardini is a freshwater species maintained in lab culture (source strain Sciento 215). The library was prepared from adults and juveniles and was constructed in pSPORTI vector (Superscript, Invitrogen) using GeneRacer (Invitrogen) Bdinburgh. Sequencing was performed by Frances Thomas, University of Edinburgh."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   814
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                                                   Contact: Blaxter ML
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
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dev stage="mixed (adult and juvenile)"
clone_lib="Hypsibius dujardini mixed stage 5'capped
(fraction 4)"
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Tel: +44 131 650 6760
Fax: +44 131 650 6760
Email: mark.blaxter@ed.ac.uk
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Unpublished (2003)
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Search completed: January 19, 2005, 16:36:47 Job time : 3915 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Sequence 25, Appl
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Sequence 33267, A
Sequence 22314, A
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Sequence 38184, A
Sequence 38576, A
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Sequence 3232,
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Sequence 100, Sequence 7, App
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## ALIGNMENTS

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WESULT INCOLOR APPLICATION US/10169953

Sequence 1, Application US/10169953

Sequence 1, Application US/10169953

Sequence 1, Application NO: US20030044915A1

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TITLE OF INVENTION: UNTRER: 2002-07-03

FRIOR TILING DATE: 2000-01-04

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LENGTH: 1035

TYPE: DAA

ORGANISM: Riebsiella pneumoniae

PRATURE:

MAMENEXY: CB

OCHER INFORMATION: P40

US-10-16-953-1

Query Match

Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2

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TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
COMPOSITION CONTAINING IT AND PREPARATION PROCESS
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
CORRESPONDENCE: Gordon W. Hueschen
STREET: 715 The "H" Bldg., 310 East Michigan
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REGISTRATION NUMBER: 16,157
REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-382-030
INFORMATION FOR SEQ ID NO: 13:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/091,257
FILING DATE: 05-Mar. 2002
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/721,979A
FILING DATE: October 4, 1996
APPLICATION NUMBER: FR 94 04009
FILING DATE: 06-APR-1994
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100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                             N'Guyen, Ngoc Thien
Baussant, Thierry
Trudel, Michel
                 Sequence 13, Application US/10091257
Publication No. US20030064078A1
GENERAL INFORMATION:
APPLICANT: Binz, Hans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
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LENGTH: 1008 base pairs
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STRANDEDNESS: single
TOPOLOGY: linear
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OTHER INFORMATION:
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COMPUTER READABLE FORM:
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Matches 1008; Conservative
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US-10-091-257-13
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                                                                                                                                                                                             Length
                                                                                                                                                                                           Score 724.4; DB 9;
Pred. No. 5.4e-226;
0; Mismatches 1;
 PRIOR APPLICATION NUMBER: 08/304,732
PRIOR FILING DATE: 1994-09-12
NUMBER OF SEQ ID NOS: 177
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 11
LENGTH: 730
                                                                                                                                                                                                                            0;
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Best Local Similarity 99.9
Matches 725; Conservative
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US-09-452-599-11
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Batent No. US20020055101A1

GENERAL INFORMATION:

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US-10-121-120-11
Sequence 11, Application US/10121120
Publication No. US20030180733A1
GENERAL INFORMATION:
APPLICANT: Bergeron, Michel G.

us-09-913-772-1.rnpb

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Pred. No. 1.2e-216;
0; Mismatches 153;
                                                                                                                                                                                                                         APPLICANT: HAREL, Jos, e
APPLICANT: BERAL, Sadjia
TITLE OF INVENTION: ARRAY AND USES THEREOF
FILE REFERENCE: 86369-3
CURRENT APPLICATION NUMBER: US/10/425,821
CURRENT FILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 176
SEQ ID NO 69
LENGTH: 1422
                                                                                                                                               Sequence 69, Application US/10425821
Publication No. US20040219530A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 67.3%;
Best Local Similarity 82.1%;
Matches 838; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
; ORGANISM: Escherichia coli
US-10-425-821-69
          996 TAAAGG 1001
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US-10-425-821-69
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TITLE OF INVENTION: Specific and Universal Probes and Amplification
TITLE OF INVENTION: Specific and Universal Probes and Amplification
TITLE OF INVENTION: Princes
TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
CURRENT APPLICATION NUMBER: US/10/121,120
CURRENT PILING DATE: 1999-12-01
FRIOR FLIING DATE: 1999-12-01
FRIOR PELICATION NUMBER: 08/304,732
FRIOR FLIING DATE: 1999-12-01
FRIOR SEQ ID NOS: 177
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Klebsiella pneumoniae
US-10-121-120-11
                                                                                                                                                                                                                                                                                                           SEQ ID NO 11
LENGTH: 730
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APPLICANT: Wise, John G.
APPLICANT: Wise, John G.
APPLICANT: Fromknecht, Katja
TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
TITLE OF INVENTION: SPECIFICITIES
FILE REFERENCE: 37779-0004
CURRENT APPLICATION NUMBER: US/10/416,708A
CURRENT FILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: Plasmid derived from pComp containing a hexahisadine separator
OTHER INFORMATION: gene
                                                                                                   ATCCGGGTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAAC 300
                                                                                                                                                                                301 ACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGT 360
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NAME/KEY: misc binding
LOCATION: (6)..(23)
OTHER INFORMATION: target binding sequence from cauliflower mosaic virus
                      181 AACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTCGTTGACTACCTGGTTGCTAAAGGC
                                                                          ATCCCGGCTGGCAAAATCTCCGCGCTCATGGGTGAATCCAACCCGGTTACTGGCAAC
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NAME/KEXY: CDS
LOCATION: (55)..(624)
OTHER INFORMATION: ompA his tag fusion
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NAME/KEY: misc_feature
LOCATION: (1)..(600)
OTHER INFORMATION: pComp derived DNA
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NAME/KEY: misc_feature
LOCATION: (601)..(624)
OTHER INFORMATION: linker and histag
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LOCATION: (658)..(3630)
OTHER INFORMATION: pComp derived DNA
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. Sequence 23, Application US/10416708A
. Publication No. US20040161753A1
. GENERAL INFORMATION:
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; OTHER INFORMATION: lac2' fragment US-10-416-708A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin version 3.2
SEQ ID NO 23
LENGTH: 3630
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Publication No. US20040014661A1

GENERAL INFORMATION:

APPLICANT: GENERAL Inliane

APPLICANT: HAEUW, Jean-Francois

APPLICANT: HAEUW, Jean-Francois

TITLE OF INVENTION: PERIPLASMIC DOMAIN OF AN ENTEROBACTERIUM OMP PROTEIN

TITLE OF INVENTION: AND ITS USE AS CARRIER OR ADJUVANT

TITLE OF INVENTION: AND ITS USE AS CARRIER OR ADJUVANT

TITLE OF INVENTION: AND ETS US/10/432,056

CURRENT APPLICATION NUMBER: US/10/432,056

CURRENT PILING DATE: 2003-05-16

PRIOR PPLING DATE: 2000-11-16

PRIOR FILING DATE: 2000-11-17

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.1

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                      795 AGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGC
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llarity 98.8%; Pred. No. 5.8e-121;
Conservative 0; Mismatches 5;
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ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (1)..(411)
US-10-432-056-1
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US-10-432-056-1
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TYPE: DNA
ORGANISM: Artificial Sequence
PERATURE:
OTHER INFORMATION: Plasmid containing a promoter, cauliflower mosaic virus-derived
OTHER INFORMATION: target operator and reporter gene and ompA-derived separator gene
PEATURE:
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                                                                                                                                                                                                                                                                                            Score 300.6; DB 17;
Pred. No. 4.2e-87;
0; Mismatches 89;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (631)...(3603)
; OTHER INFORMATION: pComp derived DNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (661)...(1110)
; OTHER INFORMATION: lacz' fragment
US-10-416-708A-26
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 77.2%;
Matches 404; Conservative
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US-10-416-708A-26

US-10-416-708A-26

Sequence 26, Application US/10416708A

Publication No. US20040161753A1

GENERAL INFORMATION:

APPLICANT: Wise, John

TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING

TITLE OF INVENTION: SPECIFICITIES

TITLE OF INVENTION UMBER: US/10/416,708A

CURRENT APPLICATION NUMBER: US/10/416,708A

CURRENT FILING DATE: 2004-01-28

NUMBER OF SEQ ID NOS: 89

SOFTWARE: PatentIn version 3.2
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                                                                -----AACAACAATGGCCCGACCCA 215
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      CCAGTATCACGACACGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCG
                                                                                                                                                                              216 TGAAAACCAACTGGGCGCTGGTGCTTTTGGTGGTTAACCAGGTTAACCCGTATGTTGGCTT
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NAME/KEY: misc_feature
LOCATION: (1)...(600)
OTHER_INFORMATION: pComp derived DNA
                                                          171 ccadraccardacacredrircarc-
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NAME/KEY: misc_feature
LOCATION: (600)..(630)
OTHER INFORMATION: linker flag tag
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NUME/KEY: CDS
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: ompA flag
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NAME/KEY: misc_binding
LOCATION: (6). (23)
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LENGTH: 3603
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                     LOCATION: (1)._(28)
OTHER INFORMATION: cauliflower mosaic virus derived target DNA sequence
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                                                                                                                                                                  LOCATION: (64)...(608)
OTHER INFORMATION: E. coli ompA derived DNA sequence
                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (608)...(684)
OTHER INFORMATION: separation tag DNA sequence
                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEX: misc feature
LOCATION: (685)..(3660)
OTHER INFORMATION: pP2HIV1-derived DNA
                                                                                                                separation tag
                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS

COCATION: (718)..(1164)

SOTHER INFORMATION: lacZ' fragment

US-10-416-708A-9
                                                                       NAME/KEY: CDS
LOCATION: (55)..(636)
OTHER INFORMATION: OMDA
misc_binding
                                                                                                                                                 NAME/KEY: misc_feature
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RESULT 10
US-10-416-708A-62
; Sequence 62, Application US/10416708A
; Publication No. US20040161753A1
; GENERAL INFORMATION:
; APPLICANT: Wise, John G.
; APPLICANT: Fromknecht, Katja

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TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING TITLE OF INVENTION: SPECIFICITIES FILE REFRENCE: 37779-0004
CURRENT APPLICATION NUMBER: US/10/416,708A
CURRENT FILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PATENTIN version 3.2
LENGTH: 4543
                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Plasmid 2 for bacterial transcriptional activation screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 CCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCTGACTCCAAAGGCAACTACGC 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 TTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGGATCACTGACGATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3479 ATACAAAGCTCAGGGCGTTCAACTGACGGCTAAACTGGGTTACCCAATCACTGACGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 CGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.9%; Score 298.6; DB 17; Length ilarity 77.2%; Pred. No. 2.1e-86; Conservative 0; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_binding
LOCATION: (12) .. (63)
OTHER INFORMATION: zif binding site and spacer
FEATURE:
NAME/KEY: promoter
LOCATION: (68) .. (110)
OTHER INFORMATION: weak promoter
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (3198)..(3782)
OTHER INFORMATION: ompA separation tag fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: terminator
LOCATION: (800)..(847)
FEATURE:
NAME/KEY: misc_binding
LOCATION: (3068)..(3119)
OTHER INFORMATION: zif binding and spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (3861)..(4310); OTHER INFORMATION: lac2' fragment US-10-416-708A-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (137)..(799)
OTHER INFORMATION: HIS3 fragment
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (3124)..(3166)
OTHER INFORMATION: weak promoter
                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 402; Conservat
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951 CCTGATCGATTGCCTGGCTCCGGGATCGTCGTGGAGATCGAAGTTAAAGGCTACAAAGA 1010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        843 TTACACGGACCGTATCGGTAAAGAAGCTTCAAACTTTAAAACTTTCACAACGTCGTGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            663 TCAAGGIGCGGCACCGGTTGCAGCTCCGGCAGTTGAAAAACTTCGCATTCAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             474 GGAATACCAGTGGGTTAACAACATCGGCGACGGGGCACTGTGGGTACCCGTCCTGATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           711 TCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                831 GTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   891 CATGGGTGAATCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 483 TTCTTTAATTTTAGGTGCGGGTGTTGAGTACGCAATTCTTCCTGAATTAGCGGCACGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1095;
APPLICATION TO BAVID, et al.
TITLE OF INVENTION: Auti-Bacterial Vaccine Compositions
FILE REFERENCE: 2034/100435;
CURRENT APPLICATION NUMBER: US/09/809,665A
CURRENT FILING DATE: 2001-03-15
PRIOR PILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 197
SEQ ID NO 150
LENGTH: 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.6%; Score 161; DB 11; 56.4%; Pred. No. 1.2e-41; iive 0; Mismatches 260;
                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 56.4
Matches 340; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Omp5-2
NAME/KEY: CDS
LOCATION: (1)..(1092)
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                                              ------certrangeraaaaccacaacaccacacrircrecaererreced
                                                                                                                                        3644 IGTTGAGTACGCGATCACTCCTGAAATCGCTACCCGTCTGGAATACCAGTGGACCAACAA 3703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTTACCCGATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCGATGGTTTGGCGC 351
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        375 TTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCAGTATTTGCTGGCGG
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Pred. No. 2.1e-60;
0; Mismatches 75; Indels
                                                                                                                                                                                                      3704 CATCGGTGACGCACACACATCGGCACTCCGGCACAACG 3744
                                                                                                                                                                                495 CATCGCCGACGCGCCACTGTGGGTACCCGTCCTGATAACG 535
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APPLICANT: Zhong, Pingyu
APPLICANT: Zhong, Pingyu
APPLICANT: Zhong, Pingyu
APPLICANT: Wang, Xinwei
TITLE OF INVERTION: ADAPTER-DIRECTED DISPLAY SYSTEMS
FILE REFERENCE: 13403.0005NPUS00
CURRENT APPLICATION NUMBER: US,10/033,399B
CURRENT FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VERSION 3.1
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US-09-809-665A-150
Sequence 150, Application US/09809665A
Publication No. US20040110268A1
                                                                                                                                                                                                                                                                                                         US-10-033-399B-24
Sequence 24, Application US/10033399B
Publication No. US20030104355Al
GENERAL INFORMATION:
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Best Local Similarity 76.3%;
Matches 289; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 24
LENGTH: 3817
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NUMBER OF SEQ ID NOS: 96
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; LOCATION: (614)..(1705)
US-10-770-824-7
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AGT 1085
AGT 1013
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1011
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                                                                                                                                                                      Compositions
                                                                                                                      GENERAL INFORMATION:

TITLE OF INVENTION: Anti-Bacterial Vaccine Conformation of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Inven
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                                                   Sequence 150, Application US/10854299 Publication No. US20050003512A1 GENERAL INFORMATION:
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Matches 340; Conservative
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US-10-854-299-150
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                                                                                                                  APPLICANT: Campos, Manuel
APPLICANT: Rosey, Everett
APPLICANT: Ankenbauer, Robert
APPLICANT: Marren-Stewart, Lynn
APPLICANT: Warren-Stewart, Lynn
APPLICANT: Keach, Robin
TITLE OF INVENTION: NOVEL PROTEINS FROM ACTINOBACILLUS PLEUROPNEUMONIAE
FILE REFERENCE: PC9854A
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Pred. No. 5.1e-41;
0; Mismatches 261; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Actinobacillus pleuropneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/770,824 CURRENT FILING DATE: 2004-02-03 PRIOR APPLICATION NUMBER: US/09/418,980 PRIOR FILING DATE: 1999-10-14
Sequence 7, Application US/10770824 Publication No. US20040198954A1 GENERAL INFORMATION:
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56.2%;
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Best Local Similarity 56.2
Matches 339; Conservative
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CCTGATCGATTGCCTGGCTCCGGATCGTCGTGAGATCGAAGTTAAAGGCTACAAAGA 1010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 AAATACACAAATCACGGAGCTCACTTAAGCTTAAAAGCAAGTTATCCAGTGCTTGAAGGA 348
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                                                                                                                                                                                    Sequence 20, Application US/10336840
Publication No. US20030219454A1
GENERAL INFORMATION:
APPLICANT: TERRY, TAMSIN DEBORAH
APPLICANT: TOBB, RHONDA JUY
APPLICANT: JENNINGS, MICHAEL PAUL
APPLICANT: JENNINGS, JOHN
TITLE OF INVENTION: HAEVAGGLUTININ ANTIGEN
TITLE OF INVENTION: HAEVAGGLUTININ ANTIGEN
CURRENT APPLICATION NUMBER: US/10/336,840
CURRENT FILING DATE: 2003-01-06
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/AU01/00822 PRIOR FILING DATE: 2001-07-06 NUMBER OF SEQ ID NOS: 39 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Haemophilus paragallinarum
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49.8%;
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Best Local Similarity 49.8
Matches 500; Conservative
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AGT 1698
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US-10-336-840-20
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                                                                                                                                                                          697 TTTGGTAAAGCAAATTTACGTCCAGAAGCACAAAATGTATTAGACGGTATTTATGGTGAA
                                589 GGTTCTGTAACTGCTGGTTTA------TCTTACCGTTTTGGTCAAAGTGCACA
                                                                                                     637 GTTGTTGAACCTAAGGTTGTTGCAAAAACATTTGCATTAAATTCAGATGTTACTTTCGCA
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547 CIGGGCGITICCIACCGCITCGGICAGGAAGAIGCIGCACCGGTTGTTGCTCCGGCTCCG
                                                                     GCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAAC
                                                                                                                                      667 TICAACAAAGCTACCCIGAAACCGGAAGGICAGCAGGCICIGGAICAGCIGIACACTCAG
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Search completed: January 19, 2005, 18:13:24 Job time : 677 secs

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	January 19, 2005, 13:35:28; Search time 116 Seconds (without alignments) 6341.953 Million cell updates/sec
Title: Perfect score:	US-09-913-772-1 1035

1 atgaaagcaattttcgtact......taactcagccggcgggttaa 1035 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters: 824507 segs, 355394441 residues Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\* Issued\_Patents\_NA:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
-	1009.8	97.6	1158	4	US-09-489-039A-280	Sequence 280, App
c 2	1009.8	97.6	1251	4	US-09-489-039A-367	367
٣	1008	97.4	1008	m	US-08-721-979A-13	13, 7
4	1008	97.4	1008	4	US-09-654-289-13	13,
ß	1008	97.4	1008	4	US-09-582-876-13	13,
9	1008	97.4	1008	4	US-10-091-257-13	13,
7		97.3	1001	٣	US-08-836-500A-1	1, 7
80		97.3	1007	4,	US-09-679-750-1	i ri
0		70.0	730	7	US-08-743-637B-11	Sequence 11, Appl
70	72	70.0	730	m	US-08-526-840B-11	1
11	537	51.9	537	ო	US-08-836-500A-3	3
12		51.9	537	4	US-09-679-750-3	'n
13		44.5	1155	4	US-09-543-681A-3750	37
14	224.8	21.7	1273	-	US-07-794-731A-1	ij
15		21.7	1273	Н	US-07-794-731A-2	Sequence 2, Appli
16	216	20.9	216	m	US-08-836-500A-5	'n
17		20.9	216	4	US-09-679-750-5	Sequence 5, Appli
18		15.6	1095	4	US-09-809-665A-150	150
13	159	15.4	1922	4	US-09-418-980-7	7
20	-	15.4	159	ო	US-08-836-500A-7	Sequence 7, Appli
21	15	15.4	159	4	US-09-679-750-7	7
22	133.	12.9	1720	Н	US-08-457-997B-1	٦,
23	133.2	12.9	1720	ო	US-08-467-722A-1	۲,
24	133.	12.9	1720	4	US-09-451-184-1	Sequence 1, Appli
25	13	12.6	1830121	4	US-09-557-884-1	л 6
26		12.6	1830121	4	US-09-643-990A-1	Ч
27	130	12.6	1830121	4	US-10-329-960-1	Η,

Sequence 9, Appli	Sequence 3, Appli	Sequence 152, App	Sequence 12, Appl	Sequence 12, Appl	Sequence 13, Appl	Sequence 13, Appl	1. A	305	Sequence 2929, Ap	10,	Sequence 10, Appl	Sequence 12, Appl	Sequence 12, Appl	Sequence 14, Appl	Sequence 14, Appl	1294	Sequence 13110, A
US-09-418-980-9	US-08-476-102A-3	US-09-809-665A-152	US-08-375-241-12	PCT-US92-06617A-12	US-08-375-241-13	PCT-US92-06617A-13	US-09-790-988-1	US-09-252-991A-3024	US-09-252-991A-2929	US-08-572-447C-10	US-09-267-747-10	US-08-572-447C-12	US-09-267-747-12	US-08-572-447C-14	US-09-267-747-14	US-09-252-991A-12949	US-09-252-991A-13110
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1319	1059	1110	184	184	169	169	640681	708	711	486	486	645	645	681	681	534	819
12.5	12.3	12.1	10.6					5.6	5.6	5.5	5.5	5.5	5.5	5.5	5.5	5.4	5.4
129.8	127.2	125	110	110	92.4	92.4	69.4	57.6	57.6	9.95	9.95	56.6	9.95	9.95	9.95	26	26
28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

US-09-489-039A-280

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Patent No. 6610836
GENERAL INFORMATION:
Facett No. 6610836
GENERAL INFORMATION:
FAPLICANT: GATY Breton et. al
APPLICANT: GATY Breton et. al
TITLE OF INVENTION:
FILLE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 280
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                                                                                                                                                                                                                                                                                                                                                        Query Match
97.6%; Score 1009.8; DB 4
Best Local Similarity 99.3%; Pred. No. 5.7e-277;
Matches 1014; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-280
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975 TCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTA 1034
1165 CGTAGCGCAGGCCGCTCCGAAAGATAACACCTGGTATGCAGGTGGTAAACTGGGTTGGTC 1106
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                                             CCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCG
                                                                                                    TAACGATCAGCTTGGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTTT
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                           CCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCG
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Sequence 367, Application US/09489039A

Fatent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Preton et. al

APPLICANT: Gary Preton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 367
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                                             CGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATACCAGTGGGTTAACAA
                                                                                                     CATCGGCGACGCGGCACCGTGGGTACCCGTCCTGATAACGGCATGCTGAGCCTGGGCGT
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llarity 99.3%; Pred. No. 5.9e-277;
Conservative 0; Mismatches 7;
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-367
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Matches 1014; Conserv
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RESULT 4

US-09-654-289-13

US-09-654-289-13

Sequence 13, Application US/09654289

Patent No. 6410030

GENERAL INFORMATION:
APPLICANT: BAILS, Hans
APPLICANT: Trudel, Michel

TITLE OF INVENTION: SPRINGE FRAGMENT OF RESPIRATORY

TITLE OF INVENTION: SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL

TITLE OF INVENTION: COMPOSITION CONTAINING IT AND PREPARATION PROCESS

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESS:

ADDRESSEE: Gordon W. Hueschen
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STREET: 715 The "H" Bldg., 310 East Michigan
STREET: Avenue
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COUNTRY:
ZIP: 4900
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Sequence 13, Application US/08721979A

Patent No. 611391

GENERAL INFORMATION:
APPLICANT: Binz, Hans
APPLICANT: Baseant, Thierry
APPLICANT: Trudel, Michel
TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
TITLE OF INVENTION: OMPOSITION CONTAINING IT AND PREPARATION PROCESS
NUMBER OF SEQUENCES: 75
CORRESPONDENCES: 75
CORRESPONDENCES: 75
CORRESPONDENCES: 75
STREET: 715 The "H" Bidg., 310 East Michigan
STREET: Avenue
CITY: Kalamazoo
STATE: MI
CONTAINING IT AND PREPARATION PROCESS
CORRESPONDENCES: 75
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Pred. No. 1.8e-276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 SOFTWARE:
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100.0%; Pred. No. ...
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OTHER INFORMATION: /note= "name : P40"
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APPLICATION NUMBER: US/08/721,979A
FILING DATE: October 4, 1996
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 04009
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hueschen, Gordon W.
REGISTRATION NUMBER: 16,157
REFERENCE/DOCKET NUMBER: 16,157
REFERENCE/DOCKET NUMBER: 16,157
RELEPHONE: 616-382-0030
TELEPHONE: 616-382-0030
TELEPHONE: 616-382-0030
TELEPHONE: 616-382-0030
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Best Local Similarity 100.
Matches 1008; Conservative
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STRANDEDNESS: single
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MOLECULE TYPE: peptide
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Gordon W. Hueschen
STREET: 715 The "H" Bldg., 310 East Michigan
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ATTORNEY/ACRATION.
NAME: Hueschen, Gordon W.
REGISTRATION NUMBER: 16,157
REPERENCE/DOCKET NUMBER: PF57PCTUS/dln
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-382-0030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOEDBY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/582,876
FILING DATE: 30-Jun-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/721,979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Application US/09582876
Patent No. 6537556
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Binz, Hans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Kalamazoo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Avenue
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US-09-582-876-13
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100.0%; Pred. No. 1.8e-276;
tive 0; Mismatches 0;
                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 SOFTWARE:
                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Hueschen, Gordon W.
REGISTRATION NUMBER: 16,157
REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616-382-030
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1008 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 1..1008
; OTHER INFORMATION: /note= "name : P40"
US-09-654-289-13
                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/654,289
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/721,979
FILING DATE:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 1008; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
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N'Guyen, Ngoc Thien
Baussant, Thierry
Trudel, Michel
TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
STROYTHAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICAL
COMPOSITION CONTAINING IT AND PREPARATION PROCESS 840 987 747 927 841 GCTGGCAAAATCTCCGCTCGCGGCATGGGGTGAATCCAACCCGGTTACTGGCAAAACTCTCTGT 900 901 GACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCCGGATCGTCGTGTAGAG 960 600 687 99 661 coggaagercagegercrogarcagergracacroagergageaacarogarcogaaa 720 807 721 GACGGTTCCGCTGTTGTTCTGGGCTACACCGACGATCGGTTCCGAAGCTTACAACCAG 780 867 627 781 CAGCTGTCTGAGAAACGTGCTCAGTCGTTGTTGTTGACTACCTGGTTGCTAAAGGCATCCCG 928 GACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAG 541 GGTCAGGAAGATGCTGCACCGGTTGTTGCTCCGGCTCCGGCTCCGGCTCCGGAAGTGGCT 628 ACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAA 601 Accaagcactrcacccrcaagrcrcaacgrrcrgrrcaacrrcaacaaagcracccrcaaa CCGGAAGGTCAGCAGGCTCTGGATCAGCTGTACACTCAGCTGAGCAACATGGATCCGAAA CAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCG 868 GCTGGCAAAATCTCCGCTCGCGCATGGGTGAATCCAACCCGGTTACTGGCAACACTGT 988 ATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTAA 1035 961 ATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTAA 1008

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97.4%; Score 1008;
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TELEPHONE: 616-382-0030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                               RESULT 6
US-10-091-257-13
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                                                                                                                                        LOCATION: 1..1008

CHER INFORMATION: /note= "name: P40"

SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-582-876-13
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1008 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                          TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                      NAME/KEY:
                                                                                                                          FEATURE
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SYNCYTIAL VIRUS PROTEIN G, IMMUNOGENIC AGENT, PHARMACEUTICA! COMPOSITION CONTAINING IT AND PREPARATION PROCESS
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                                                                                                                                                                                                                       901 GACAACGIGAAAGCICGCGCIGCCCIGAICGAIIGCCIGGCICCGGAICGIGGIGIAGAG 960
781 CAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCG
                                                                                                                                                                     GACAACGTGAAAGCTCGCGCTGCCCTGATCGATTGCCTGGCTCCGGATCGTCGTGTAGAG
                                                        GCTGGCAAAATCTCCGCTCGCGGCATGGGTGAATCCAACCCGGTTACTGGCAACACCTGT
                                                                                                             841 GCTGGCAAAATCTCCGCTCGCGCATGGGTGAATCCAACCCGGTTACTGGCAACACTGT
                                                                                                                                                                                                                                                                                                               ATCGAAGTTAAAGGCTACAAAGAAGTTGTAACTCAGCCGGCGGGTTAA 1008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/10091257
Patent No. 6616930
GENERAL INFORMATION: Hans
APPLICANT: Binz, Hans
N'Guyen, Ngoc Thien
Baussant, Thierry
Trudel, Michel
TITLE OF INVENTION: PEPTIDE FRAGMENT OF RESPIRATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gordon W. Hueschen
STREET: 715 The "H" Bldg., 310 East Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hueschen, Gordon W.
REGISTRATION NUMBER: 16,157
REFERENCE/DOCKET NUMBER: PF57PCTUS/dln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/721,979A
FILING DATE: OCCOBER 4, 1996
APPLICATION NUMBER: FR 94 04009
FILING DATE: 06-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/091,257
FILING DATE: 05-Mar-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1..1008

CHER INFORMATION: /note= "name;
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-091-257-13
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APPLICANT: Baussant, Thierry
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APPLICANT: Baussant, Thierry
APPLICANT: Haew, Jean-Francois
APPLICANT: Haew, Jean-Francois
APPLICANT: Haew, Jean-Francois
APPLICANT: Mayen Mgc, Thien
TITLE OF INVENTION: Effect, Immunogenic Complex Containing It, Process for TITLE OF INVENTION: Their Preparation, Nucleotide Sequence and Vaccines
Fatent No. 6197929
NUMBER OF SEQUENCES: 8
NUMBER OF SEQUENCES: 8
NUMBER OF SEQUENCES: 8
STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
STREET: 4700
CITY: Chicago
STATE: Illinois
COUNTY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/836,500A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 97.3%; Score 1007; DB 3; I Best Local Similarity 100.0%; Pred. No. 3.4e-276; Matches 1007; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION: 424
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: KRZZ, MARTIN L.
REGISTRATION NUMBER: 25,011
REFERENCE/DOCKET NUMBER: PIEIF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1007 base pairs
...... nucleic acid
                        Sequence 1, Application US/08836500A Patent No. 6197929 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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US-08-836-500A-1
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                             Indels
    Pred. No. 1.8e-276;
Mismatches 0;
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100.0%;
    Best Local Similarity 100.
Matches 1008; Conservative
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/679,750
                                                                                FILING DATE: 08-Oct-2000
CLASSIPFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,500
FILING DATE: «Unknown»
ATORNEY/AGENT INFORMATION:
NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
REFERENCE/DOCKET NUMBER: PIE1514P0180US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 97.3%; Score 1007; DB 4; L
Best Local Similarity 100.0%; Pred. No. 3.4e-276;
Matches 1007; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1..1007
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                     TELEPHONE: 312-616-5400
                                                                                                                                                                                                                                                                                                                     LENGTH: 1007 base pairs
                                                                                                                                                                                                                                                                   TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
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STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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US-09-679-750-1
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Pred. No. 5.2e-196;
0; Mismatches 1;
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; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
                                                                                                                  Klebsiella pneumoniae
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Klebsiella pneumon
US-08-743-637B-11
                                                                                                                                                                                  70.0%;
                                                                                                                                                                               Query Match
Best Local Similarity 99.9
Matches 725; Conservative
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US-08-526-840B-11
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                                                     ACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAGCTACCTGAAA
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                              ACCAAGCACTTCACCCTGAAGTCTGACGTTCTGTTCAACTTCAACAAAGCTACCCTGAAA
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,637B
FLING DATE: 04-NOV-1996
CLASSIFICATION: 435
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APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
APTING DATE: 11-SEP-1995
APTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 95,0012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETTE, Marc
APPLICANT: OUELLETTE, Marc
APPLICANT: OUELLETTE, Marc
APPLICANT: OUELLETTE, Marc
APPLICANT: OUELLETTE, Marc
APPLICANT: PICARD, M.
TITLE OF INVENTION: SPECIES-SPECIFIC A
TITLE OF INVENTION: DERDIFFY COMMON BA
TITLE OF INVENTION: IDENTIFY COMMON BA
TITLE OF INVENTION: ANTIBIOTIC RESISTA
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
STREET: 411 EAST MISCONSIN AVENUE
CITY: MILMAUKEE
STREET: 411 EAST MISCONSIN AVENUE
CITY: MILMAUKEE
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/08743637B; Patent No. 5994066; GENERAL INFORMATION:
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(414) 277-5591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: BERGER
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US-08-743-637B-11
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600

935 9 995 720

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GENERAL INFORMATION:

APPLICANT: Baussant, Thierry
APPLICANT: Baussant, Thierry
APPLICANT: Haeuw, Jean-Francois
APPLICANT: Haeuw, Jean-Francois
APPLICANT: Wouyen Ngoc, Thien
TITLE OF INVENTION: Effect, Immunogenic Complex Containing It, Process for TITLE OF INVENTION: Effect, Immunogenic Complex Containing It, Process for TITLE OF INVENTION: Their Preparation, Nucleotide Sequence and Vaccines Patent No. 6197929
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
                                                             815
                                                                                                                                                                                                                  TGAGAAACGTGCTCAGTCCGTTGTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAA 875
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPPY disk
COMPUTER: PROPERATIONE
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,500A
FILING DATE:
CLASSIFICATION: 424
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REGISTRATION NUMBER: 25,011
RESERENCE/DOCKET NUMBER: PIE1514P0180US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEPRAX: 312-616-5460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 3, Application US/08836500A; Patent No. 6197929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAX: 312-616-5460
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 537 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
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STATE: Illinois
COUNTRY: U.S.A.
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                            AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
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       SPECIFIC AND UNIVERSAL PROBES AND
                                                                                                                                                                                                                                                ZIP: 52202-4497

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Patent Pec-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REGISTRATION INFORMER: 85.056.90012
TELECOMMUNICATION INFORMATION:
TITLE OF INVENTION: SPECIFIC AND UNIVE
TITLE OF INVENTION: AMPLIFICATION PRIM
TITLE OF INVENTION: COMMON BACTERIAL P
TITLE OF INVENTION: COMMON BACTERIAL SPECTORESPONDENCES: 177
CORRESPONDENCE ADDRESS: 177
ADDRESSEE: QUARLES & BRADY
STREET: 411 East Wisconsin Avenue
CITY: Milwankee
STATE: Wisconsin
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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 730 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 99.9
Matches 725; Conservative
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STRANDEDNESS: double
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Sequence 3750, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGACGGCCGTCGACCGTAACGATCAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTTCGAAATGGGTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 GACTGGCTGGGCCGTATGGCATATAAAGGCAGCGTTGACAACGGTGCTTTCAAAGCTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 ACCGGTTTCTACGGTAACGGTTTCCAGAACAACAACGGTCCGACCCGTAACGATCAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTTTCGAAATGGGTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 537;
             PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/836,500
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
REFERENCE/DOCKET NUMBER: PIE1514P0180US
TELEPONE 312-616-5400
TELEPAN: 312-616-5400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
IENGTH: 537 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
51.9%; Score 537; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 7.5e-143;
Matches 537; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1..537
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                              GETGCTGGTGCGTTCGGTGGTTACCAGGTTAACCCGTACCTCGGTTTCGAAATGGGTTAT 180
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AL INFORMATION:
APPLICANT: Binz, Hans
Baussant, Thierry
Hauw, Jean-Francois
Hauw, Joan-Francois
TITLE OF INVENTION: Carrier Protein Having an Adjuvant
Effect, Immunogenic Complex Containing It, P
Their Preparation, Nucleotide Sequence and 1
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0
                                                         51.9%; Score 537; DB 3; Length 537;
100.0%; Pred. No. 7.5e-143;
.ive 0; Mismatches 0; Indels
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NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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APPLICATION NUMBER: US/09/679,750
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STATE: Illinois
COUNTRY: U.S.A.
                                                                               Best Local Similarity 100.
Matches 537; Conservative
LOCATION:
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US-08-836-500A-3
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US-09-679-750-3
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1017
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                                                                                                                                           1018 AAAGAAAACCCAGTAACTGGCAACACTTGTGACAACATCAAAGCTCGTGCAGCTCTGATC 1077
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                                            958 Grigariachggranchaaagmarrcchgcaacacarchchgcagaagmegre
                                                                                              898 GAATCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATC
  GTTGACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 TTAACCCGTATGTTGGCTTTGAAATGGGTTACGACTGGTTAGGTCGTATGCCGTACAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: George Georgiou
APPLICANT: Joseph A. Francisco
APPLICANT: Charles F. Barhart
TITLE OF INVENTION: Expression of Proteins on Bacterial
TITLE OF INVENTION: Surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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0; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/794,731A
FILING DATE: 19311115
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 1, Application US/07794731A; Patent No. 5348867; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION UNDHER: 33,928
REFERENCE/DOCKET UNDHER: GEOG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 370-7200
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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78.0%;
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
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Matches 290; Conservative
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CORRESPONDENCE ADDRESS:
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US-07-794-731A-1
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US-07-794-731A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             418 GACGITIATACACGITIAGGIGGIATGGCGIGCAGATICAACIGCAACIAITAAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376 TCTACCGGCGTTTCCCCGT-----AGCGAACACGACACGCGTTTCCCCCAGTA
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                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                          Length 1155;
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                          Score 460.4; DB 4;
Pred. No. 5.8e-121;
0; Mismatches 321;
DIAGNOSTICS AND THERAPEUTICS
         FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR PILING DATE: 1999-4-09
NUMBER: OF SEQ ID NOS: 8344
SEQ ID NO 3750
LENGTH: 1155
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 67.1%;
Matches 691; Conservative
                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-3750
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                      112 ACCCAATCACTGACGACCTGGACATCTACACTCGTCTGGGTGGCATGGTATGGCGTGCAG
                                                                                                                                            416 CCCCAGTATTTGCTGGCGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGG
                                                                                                                                                                                                                 476 AATACCAGTGGGTTAACAACATCGGCGACGCGGGCACTGTGGGTACCCGTCCTGATAACG
                                                                      356 ACTCCAAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTT
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                                    415
                                                         CTCCGGTCTTCGCTGGCGGTGTTGAGTACGCGATCACCCCTGAAATCGCTACCCGTCTGG 376
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212 ACCCAATCACTGACGACCTGGACATCTACACTCGTCTGGGTGGCATGGTATGGCGTGCAG 271
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                                  ACTCCAAAGGCAACTACGCTTCTACCGGCGTTTCCCCGTAGCGAACACGACACTGGCGTTT
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/07794731A;
Patent No. 5348867;
GENERAL INFORMATION:
APPLICANT: George Georgiou
APPLICANT: Jeorge Georgiou
APPLICANT: Jeanles F. Earhart
TITLE OF INVENTION: Expression of Proteins on Bacterial
TITLE OF INVENTION: Surface
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Annold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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Pred. No. 4.8e-54;
0; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC CDOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/794,731A
FILING DATE: 19911115
CLASSIFICATION: 435
ATTORNEY/ACTIVE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTATION NUMBER: 33,928
REFERNCE/DOCKET NUMBER: GEOG:001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 320-7200
TELEPHONE: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.7%;
78.0%;
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
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Best Local Similarity 78.0
Matches 290; Conservative
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COUNTRY: US
ZIP: 77210
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US-07-794-731A-2
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US-07-794-731A-2
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Novel

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Acf65985 Photorhab Aba91422 Haemophil Aas82075 DNA encod Aas82046 DNA encod

Aat31610 Klebsiell

us-09-913-772-1.rng

Perfect score:

ritle:

Sequence:

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database :

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Use of membrane fractions from Gram-negative bacteria as immunostimulants for the treatment or prevention of cancer, increases effect of e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes a P40 polypeptide of Klebsiella pneumoniae. The protein is found in the membrane fraction, and is used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                  P40; membrane fraction; Gram-negative bacteria; anticancer; immune response; mononuclear blood cell; tumour necrosis factor-alpha; interleukin-12; antitumour; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding a P40 polypeptide of Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bonnefoy J;
                                                    ACF68624
ACF67367_13
ACF65379
ABN83312
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                                                                                             AAD40179
AAD40180
AAD40168
AAD40198
AAD40199
AAD14893
AAD14893
AAC79663
AAC79663
AAC79663
                                           ADF03465
                                                                                                                                                                                                                  ACF65985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 25-27; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .1035
/*tag= a
/product= "P40"
                       AAT31608
                                AAQ02030
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                                                                                                                                                                                                                                                                                                                                   AAA96568 standard; DNA; 1035 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beck A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAR-2000; 2000WO-FR000623.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-587477/55.
P-PSDB; AAB18994.
                                                              WO200054790-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-1999;
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642.4
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224.8
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   Aaa7888 DNA encod
Aaa63956 DNA encod
Aah74731 Nucleotid
Aaf80152 Nucleotid
Aav13868 Gene codi
Aaf86153 Nucleotid
Aaa78461 Nucleotid
Aah78461 Nucleotid
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Ach94572 Klebsiell
Aav13867 Gene codi
Aat31607 Klebsiell
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Aaa75881 DNA encod
Aaa63956 DNA encod
Aah74731 Nucleotid
Aaf80152 Nucleotid
Aav13868 Gene codi
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Aat28425 K.pneumon
Aba76835 Klebsiell
Aag02032 Plasmid p
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Aaa63961 DNA encod
Aaa15498 DNA encod
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9010.200 Million cell updates/sec
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                                                                        Search time 603 Seconds
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                                                                                                                                                                                                                8269772
           GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                            4134886 segs, 2624710521 residues
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Listing first 45 summaries
                                                   nucleic search, using sw model
                                                                        January 19, 2005, 10:15:18
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AAH78461
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match Length DB
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Result No.

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fraction from Gram-negative bacteria for the preparation of an immunostimulating composition that can induce an anticancer immune response. The membrane fraction not only stimulates proliferation of human mononuclear blood cells (immunostimulation) but also induces production of tumour necrosis factor-alpha and interleukin (IL)-12, which are known to have antitumour activity, so that it improves the effects of other co-administered anticancer treatments (chemotherapy or radiation). The membrane fraction is used for treatment and prevention of cancer (particularly of the bladder, prostate, colon or liver) and also
The specification describes the use of
                                                                                                                                                                                                                                                                                  malignant melanomas
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Sequence 1035 BP; 227 A; 283 C; 288 G; 237 T; 0 U; 0 Other;

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The present sequence encodes a Klebsiella pneumoniae outer membrane protein A (OmpA), designated P40. The enterobacterial OmpA polypeptide, or its fragments, is used for preparing a composition that induces, or increases, the cytotoxic T cell (CTL) response against an infectious agent or tumour cell. Compositions containing OmpA, optionally mixed with or coupled to a suitable antigen or hapten, are used as vaccines for treatment or prevention of infections caused by viruses, bacteria, fungi and parasites or tumors, particularly where associated with an antigen and specifically melanoma. Nucleic acids that encode OmpA (or its fusion with antigens or haptens) are useful as genetic vaccines again for

Sequence 1035 BP; 227 A; 283 C; 288 G; 237 T; 0 U; 0 Other;

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tumour-associated antigen; autoimmune disease; allergy; graft rejection;
cardiovascular disease; central nervous system disease; inflammation;
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                                                                                                                                                                                                          DNA encoding a Klebsiella P40 protein.
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                                                   P40; outer membrane protein A; OmpA; immunogen; cytokine; growth factor; hormone; tumour-specific marker; vaccine; cancer; contraceptive; ss.
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                                                                                                                                                                                                                                                                                                            ebsiella membrane fraction as adjuvant, for e.g. antitumor or vaccines, to direct a Th1, or mixed, immune response against
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                                                                                                                                                                   N'guyen TN, Beck A,
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The present sequence encodes a Klebsiella pneumoniae outer membrane protein A (OmpA), designated P40. The enterobacterial OmpA polypeptide, or its fragments, is used for preparing a composition that induces, or increases, the cytotoxic T cell (CTL) response against tumour cells. Compositions containing OmpA, optionally mixed with or coupled to a suitable antigen or hapten, are used as vaccines for treatment or prevention of tumors, particularly where associated with an antigen and specifically melanoma. Nucleic acids that encode OmpA (or its fusion with antigens or haptens) are useful as genetic vaccines again for treating
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Best Local Similarity 100.0%; Pred. No. 3.5e-283;
Matches 1035; Conservative 0; Mismatches 0;
Example 1; Page 28-29; 35pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Outer membrane protein A; P40; antigen presenting cell; vaccine; antiviral; antibacterial; anticancer; autoimmune disease; inflammation; graft rejection; cardiovascular disease; immune deficiency; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preparing purified polypeptide soluble in absence of detergent, useful for modulating the immune system, e.g. in vaccines, by removal of detergent, denaturing and molecular sieving.
CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTTGTT
                      CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCGGTTGTT
                                                                           GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA
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human immune deficiency virus, respiratory syncytial virus, measles, mumps, tuberculosis etc.), but also against fungi, parasites, autoimmune diseases, graft rejection, cardiovascular disease, inflammation and immune deficiency
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                                                                                                                                                                                                                                                                                                                                        Outer membrane protein A; OmpA; P40; enterobacteria; nasal composition; respiratory syncytial virus; RSV; RSV infection; lung; respiratory tract;
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TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT
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Best Local Similarity 100.0%; Pred. No. 2.4e-282;
Matches 1032; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The patent discloses a new immunogenic complex which consists of (1) an oligo- or polysaccharide found naturally on bacteria, coupled to (2) a carrier protein chosen from (a) the human serum albumin binding protein of Streptococcus, (b) Gram-negative bacterial outer membrane proteins of Streptococcus, (b) Gram-negative bacterial outer membrane proteins (0mp), or (c) fragments of these proteins. The immunogenic complex is useful in a vaccines to protect animals against infection by Salmonella, especially those belonging to antigenic specificity group 0:9, including S. enteritidis, S. panama and S. dublin. A vaccine prepared using an oligosaccharide from S. enteritidis can be used to provide protection against septicaemia caused by S. typhi and against typhoid fever, as well as to protect humans and animals from toxic infections and zoonosis caused by Salmonella of the same serogroup. The carrier proteins enhance the immunogenicity of the oligo- or polysaccharide antigens. Inclusion of additional Salmonella capsule antigens, such as the Vi antigen, increases the vaccine's efficacy against encapsulated bacteria. The present sequence represents a gene coding for LP40, a preferred example of a carrier protein which can be used in the immunocomplex. LP40 is a variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein from the outer membrane protein of Klebsiella
I-145. The gene can be used for recombinant expression of LP40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic complex for use in anti-bacterial vaccine - comprises bacterial oligo; or poly:saccharide coupled to a Gram-negative bacterial outer membrane protein or a Streptococcal HSA binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                              for LP40, a variant of OmpA protein P40 from K. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGAAAGCAATTTTCGTACTGAATGCGGCTCCGAAAGATAACACCTGGTATGCAGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                       Outer membrane protein; OmpA; LP40; immunocomplex; oligosaccharide; polysaccharide; vaccine; Salmonella; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane protein of Klebsiella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1030.2; DB 2; Length
Pred. No. 8e-282;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .1035
/*tag= a
/product= "LP40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 36-38; 63pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FABR ) FABRE MEDICAMENT SA PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haeuw J, Svenson S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-FR000800.
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                                             (first entry)
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                                                                                                                                                                                                                                  pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                  WO9741888-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAY-1996;
                                                                                         Gene coding
                                                16-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                           13-NOV-1997
                                                                                                                                                                                                          Synthetic.
Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the P40
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AAV13868;
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ATCACTGACGATCTGGACATCTACACCCGTCTGGGCGGCATGGTTTGGCGCGCGTGACCCC
                                                                           GTATTTGCTGGCGGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC
                                                                                                                                                                                                                           CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGTTGCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 721 ACTCAGCTGAGCAACATGGATCCGAAAGACGCTTCCGCTGTTGTTCTGGGCTACACCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   961 TGCCTGGCTCCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT
                                                                                                                                                                                                      CAGTGGGTTAACAACATCGGCGACGCGGCACTGTGGGTACCCGTCCTGATAACGGCATG
                                                                                                                                                                                                                                                                                                                                                    GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG
                                                                                                                                                                                                                                                                                                                                                                                      601 Gerecegerecegerecegaagregeraceaageacrreacereaagrereaefrere
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                                                                                                                                                     GTATTTGCTGGCGCGCGTAGAGTGGGCTGTTACTCGTGACATCGCTACCCGTCTGGAATAC
                                                                                                                                                                                                                                                                              CTGAGCCTGGGCGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG
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                                                          AAAGGCAACTACGCTTCTACCGGCGTTTCCCGTAGCGAACACGACACTGGCGTTTCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JAN-2000
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                      301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes a fusion protein comprising a Klebsiella pneumoniae outer membrane protein A (OmpA) designated P40 and a respiratory syncytial virus (RSV) antigen. Bnterobacterium OmpA proteins, associated with an immunogenic peptide from RSV are used to prepare a nasal composition that induces a protective response, against RSV infection in the upper and lower (lung) respiratory tract. OmpA potentiates the immune response to some immunogenic peptides, eliminating the need for adjuvants. The method is useful for producing vaccines for prevention or treatment of RSV infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine against respiratory syncytial virus, comprises enterobacterial outer membrane protein and viral immunogen, provides protective response throughout the respiratory tract.
                                       r membrane protein A; OmpA; P40; enterobacteria; nasal composition;
RSV infection; lung; respiratory tract; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTGACAACGCTGCTTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAACTGGGTTGGTCCCAGTATCACGACACCGGTTTCTACGGTAACGGTTTCCAGAACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACGGTCCGACCCGTAACGATCAGCTTGGTGCTGGTGCGTGGTTACCAGGTTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTACCTCGGTTTCGAAATGGGTTATGACTGGCTGGGCCGTATGGCATATAAAGGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                         P40 and RSV antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 1356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
     sequence of a fusion protein of P40 and RSV antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1356 BP; 350 A; 397 C; 343 G; 266 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1026.2; DB 4;
Pred. No. 1.2e-280;
0; Mismatches 3;
                                                                                                                                                                                            1. .1356
/*tag= a
/product= "fusion protein of "
/note= "no termination codon"
                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 29-31; 39pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                           (FABR ) FABRE MEDICAMENT SA PIERRE.
                                                                                                                                                                                                                                                                                                                                                    2000WO-FR002626.
                                                                                                                                                                                                                                                                                                                                                                                        99FR-00011888.
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ilarity 99.7%;
Conservative
                                                                                                                                syncytial virus.
                                                                                                             pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corvaiea N, Goestch
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Matches 1028; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAB67771.
                                                                                                                                                                                                                                                                              WO200121203-A1
                                                                                          Synthetic.
Klebsiella pr
Respiratory
                                                                                                                                                                                                                                                                                                                                                      22-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                        23-SEP-1999;
                                                                                                                                                                                                                                                                                                                  29-MAR-2001
     Nucleotide
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                                                                                                                                                                 TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC
                         GCTCCGGCTCCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG
                                                                                                                                                                                             TTCAACTTCAACAAAGCTACCCTGAAACCGGAAGGTCAGCAGGCTCTGGATCAGCTGTAC
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    CTGAGCCTGGGGGTTTCCTACCGCTTCGGTCAGGAAGATGCTGCACCGGTTGTTGCTCCG
                                                                                  GCTCCGGCTCCGGCTCCGGAAGTGGCTACCAAGCACTTCACCCTGAAGTCTGACGTTCTG
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IgG response; tumour; viral infection; bacterial infection;
parasitic infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of a Klebsiella protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH78461 standard; DNA; 1032 BP.
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                                                                                                                                                                                                                                                                                                   The invention relates to the use of a fragment of a bacterial membrane protein, especially the outer membrane protein from an enterobacterium, e.g. the CompA protein from Klebsiella pneumoniae, in a composition for nasal administration to improve immunity, in mammals, against an antigen or hapten. The antigen or hapten is derived from bacteria and viruses that cause respiratory infections e.g. the human or bovine respiratory syncytial virus. This sequence corresponds to the gene encoding the OmpA protein from Klebsiella. The antigens are shown in AAV44078-Y44149 [AAZ30478-Z30538 for coding sequences). The use of a membrane protein, from a species other than that from which the antigen is derived, induces a protective response against the antigen, even without an adjuvant, since most adults will already be sensitized against the membrane protein, protein, although the membrane protein-antigen product will induce an anti-membrane protein response even in subjects who are not pre-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                  Immunogenic composition containing bacterial outer membranr protein conjugated or fused to antigen or hapten, for nasal administration,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.9%; Score 1024; DB 2; 99.5%; Pred. No. 4.6e-280; ive 0; Mismatches 5;
                                                                              Nguyen TN, Haeuw JF,
                                                                                                                                                                                                                             protect against respiratory pathogens.
                                                                                                                                                                                                                                                               Disclosure; Page 17-18; 64pp; French.
                                      (FABR ) FABRE MEDICAMENT SA PIERRE
  98FR-00003814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 99.5
Matches 1027; Conservative
                                                                              Rauly I,
                                                                                                                       WPI; 1999-583089/50.
                                                                                                                                            P-PSDB; AAY44077
27-MAR-1998;
                                                                              Andreoni C,
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The present sequence encodes a recombinant outer membrane protein A, designated rP40. The specification describes a method for the recombinant production of a protein, or its fragments. The method comprises renaturation the protein, after extraction, in the presence of a solution containing one of the detergents Zwittergent 3-14, Zwittergent 3-12 and cotylquocopyranoside, where the protein is not beta-interferon. The protein is especially the outer membrane protein (OMP) from an encobacterium, and is useful as a carrier for delivering antigens or hathogens of the respiratory tract, e.g. respiratory syncytial virus (RSV), (para) influenza, hanta virus, Streptococci, Pheumococci and Meningococci, especially human or bovine RSV. Most adults show an tribody response to the Klebsiella pneumoniae P40, and this presensitisation stimulates the immune response to an antigen/hapten conjugated to the protein
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                                          The present sequence encodes a Klebsiella protein. The protein is administered to test the adjuvant effect of zwitterionic detergents. The apecification describes the use of zwitterionic detergents in the preparation of a mucosally administered pharmaceutical composition for inducing or improving the immune response of a mammal towards an antigen or hapten. In presence of zwitterionic detergents, vaccines are effective on mucosal (especially nasal) administration, which has the general advantages of inducing specific IgA production directly at the site of infection, stimulating a systemic IgG-type response (creating a secondary barrier against infection) and being simpler to carry out than administration by injection. The pharmaceutical composition is specifically a vaccine for the treatment or prophylaxis of tumours or viral, bacterial or parasitic infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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98.9%; Score 1024; DB 4;
Best Local Similarity 99.5%; Pred. No. 4.6e-280;
Matches 1027; Conservative 0; Mismatches 5;
  Disclosure; Page 20-21; 26pp; French.
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                                                                                                                     TCCAACCCGGTTACTGCCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT
                                                                                                                                                                                                                         901 TCCAACCCGGTFACTGGCAACACTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of a recombinant outer membrane protein A (rP40)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF90077 standard; DNA; 1032 BP
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TGCCTGGCTCCGGATCGTCGTGTAGAGATCGAAGTTAAAGGCTACAAAGAAGTTGTAACT 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTCAAAGCTCAGGGCGTTCAGCTGACCGCTAAACTGGGTTACCCGATCACTGACGATCT 314
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    expression vector; transcription regulatory element,
pneumoniae protein; antibacterial; Vaccine; gene; ds

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1158 BP; 259 A; 315 C; 322 G; 262 T; 0 U; 0 Other;
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Pred. No. 5.1e-276;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                  Klebsiella pneumoniae polynucleotide segid 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENO-) GENOME THERAPEUTICS CORP.
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The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element, and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This sequence encodes a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                           useful for
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Pred. No. 5.3e-276;
0; Mismatches 7; Indels 0;
                                                                                                                                                                                          New nucleic acid encoding a Klebsiella pneumoniae polypeptide, preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                          Seguence 1251 BP; 282 A; 346 C; 348 G; 275 T; 0 U; 0 Other;
                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 367; 932pp; English
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                               27-JAN-2000; 2000US-00489039
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Matches 1014; Conservative
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Klebsiella pneumoniae protein; antibacterial; Vaccine; gene; ds.
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## ALIGNMENTS

BD260130 1035 bp DNA linear PAT 17-JUL-2003 Use of an enterobacterium protein OmpA for specific targeting

cowards antigen-presenting cells.

BD260130.1 GI:33069900

C07K14/26, C07K19/00, C12N5/06, C12N15/09, A61K37/02, C12N15/00, PC

THIERRY BAUSSANT A61K39/00,A61K35/76,A61K39/02,A61K39/385,A61K39/39,A61K48/00, AGIP25/00,AGIP29/00,AGIP31/00,AGIP35/00,AGIP37/02,AGIP37/04, AGIP37/06,

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Use of an enterobacterium protein OmpA for specific targeting

antigen-presenting cells Key Location/Qualifiers

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1035 /organism="Klebsiella pneumoniae"

| Xlebsiella pneumoniae | JP 2002529428-A/1 | 10.5EP-2002 | JP 200580661 | JP 2000580661 | JP 20007-1999 | JP 2000580661 | JEAN YVES BONNEFOY, SYBILLE LECOANET, JEAN PIERRE AUBRY, PASCALE

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A61K47/48,
A61F31/00,A61F31/04,A61F31/10,A61F31/12,A61F33/00,A61F35/00,
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Location/Qualifiers
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Conservative 0; Mismatches 0;
     /mol_type="genomic DNA"
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriacaea; Klebsiella.

Liboro, C., Corvaia, N., Beck, A. and Vonnefoy, J. Y.
Liboro, C., Corvaia, N., Beck, A. and Vonnefoy, J. Y.
Limunostimulant bacterial membrane fractions in cancer treatment
Patent: JP 202539170-A 1 19-NOV-2002;
PN JP 2002539170-A 1 19-NOV-2002
PN JP 2002539170-A/1
PD 19-NOV-2002
PR 15-MAR-2000 JP 2000604865
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Immunostimulant bacterial membrane fractions in cancer treatment.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
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Sequence 1 from Patent W00048629.
AX033532 GI:10280280
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QSVVDVLVAKGIPAGKISARGMGESNFVTGNNYKARAALIDCLAPDRRVBIEVKG
YKEVVTQPAG"
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Use of an enterobacterium protein ompa associated with an antigen
for generating an antiviral, antiparasitic or antitumoral cytotoxic
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Klebsiella pneumoniae
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
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                                     GACTACCTGGTTGCTAAAGGATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA
                                                                                                            TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT
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                    GACTACCTGGTTGCTAAAGGCATCCCGGCTGGCAAAATCTCCGCTCGCGGCATGGGTGAA
                                                                                         TCCAACCCGGTTACTGGCAACACCTGTGACAACGTGAAAGCTCGCGCTGCCCTGATCGAT
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Patent: WO 0048628-A 1 24-AUG-2000;
PF MEDICAMENT (FR) ; BONNEFOY JEAN YVES
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/note="unnamed protein product"

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Sequence 1 from Patent WO0048628.
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/mol type="unassigned Di
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YKEVVTQPAG"
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Klebsiella pneumoniae
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
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                                                                                                                                                                             CGCATCGGTTCCGAAGCTTACAACCAGCAGCTGTCTGAGAAACGTGCTCAGTCCGTTGTT
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                                                                                                  <u> ACTCAGCTGAGCAACATGGATCCGAAAGACGGTTCCGCTGTTGTTCTGGGCCTACACCGAC</u>
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/note="unnamed protein product"
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Patent: FR 2789902-A 1 25-AUG-2000;
PF MEDICAMENT (FR)
Location/Qualifiers
1. 1035
/organism="Klebsiella pneumc/mol_type="unassigned DNA"
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Sequence 1 from Patent FR2789902.
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AX034418.1 GI:10303128
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Use of an ompa enterobacterium protein associated Patent: WO 0048629-A 1 24-AUG-2000; MICONNET ISABELLE (CH) ; ROMERO PEDRO (CH) ; CAROT (CH) ; PF MEDICAMENT (FR) ; RENNO TOUFIC (FR) ; BC
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                                               Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Klebsiella.
                                                                                                                                    ; LIBON CHRISTINE
                                                                                          Beck, A., Libon, C., Bonnefoy, J.Y. and Corvaia, N. Immunostimulant bacterial membrane fractions in Patent: WO 0054790-A 1 21-SEP-2000;
PF MEDICAMENT (FR); BECK ALAIN (FR); LIBON CHR BONNEFOY JEAN YVES (FR); CORVAIA NATHALIE (FR)
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/organism="Klebsiella p
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Sequence 1 from Patent WO0054790. AX035661

Query Match Best Local Similarity 100. Matches 1035; Conservative	Qy 1 ATGAAAGCAATTTTCG	Db 1 ATGARAGCAITTTTCC Qy 61 AAACTGGGTTGGTTGCCC	Db 61 AAACTGGGTTGGTCCC Qy 121 AACGGTCCGACCCGTA	121	Oy 181 CCGTACCTCGGTTTCG	241 G	Db 241 GTTGACAACGGTGCTT Ov 301 ATCACTGACGATCTTGG	301 ATCACTGACGA	Qy 361 AAAGGCAACTACGCTT	Db 361 AAAGGCAACTACGCTT	Oy 421 GPATTTGCTGGCGGCG	481	Db 481 CAGTGGGTTAACAACA	Qy 541 CTGAGCCTGGGCGTTT	Db 541 CTGAGCCTGGGCGTTP	601 G	DB 601 GCTCCGGCTCCGGCTC	661	Qy 721 ACTCAGCTGAGCAACA	Db 721.ACTCAGCTGAGCAACA	Qy 781 CGCATCGGTTCCGAAG	Db 781 CGCATCGGTTCCGAAG	Qy 841 GACTACCTGGTTGCTA	Db 841 GACTACCTGGTTGCTA	OY 901 TCCAACCCGGTTACTG	901		DD 961 TGCCTGGCTCCGGATC
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Enterobacteriaceae; Klebsiella.
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Use of an outer membrane protein a of an enterobacterium awith a rsv immunogenic peptide for preparing vaccines for intransaal administration
Patent: WO 0121203-A 1 29-MAR-2001;
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Enterobacteriaceae; Klebsiella.
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1. .1035
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Sequence 1 from Patent W00149705.
AX191406.1 GI:15209619
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Submitted (04-AUG-1997) Haeuw
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/product="outer membrane protein A"
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| DDLDIYTRLGGMVWRADSKNYASTGVSRESHDTGVSPPPAGGVEWAYTRDIATRLEY
| DDLDIYTRLGGMVWRADSKNYASTGVSRESHDTGVSPPAGAVBAPAPAPAPAFTKSD
| VLFNRNKATLKFREGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSERAN
| GSVVDXLVAKGIFAGGSNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKG
| YKEVVTQPQG"
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Use of an outer membrane protein a of an enterobacterium associated with a rsv immunogenic peptide for preparing vaccines for intranasal administration
Patent: WO 0121203-A 3 29-MAR-2001;
PIERRE FABRE MEDICAMENT (FR)
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L'ADN DE KLEBSIELLA PNEUMONIAB (SEQ ID No. 1) ET
DU VIRUS RESPIRATOIRE SYNCYTIAL (SEQ ID No. 8)"
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Sequence 3 from Patent W00121203.
AX101164
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  Score 1026.2; DB 6;
Pred. No. 1.4e-239;
0; Mismatches 3;
99.1%;
99.7%;
                        Best Local Similarity 99.7
Matches 1028, Conservative
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Haeuw,J.F., N'Guyen,T., Rauly,I., Andreoni,C. and Baussant,T.
Haeuw,J.F., active p40 conjugates for nasal delivery
Patent: WO 9949892-A 1 07-OCT-1999;
HAEUW JEAN FRANCOIS (FR); GUYEN THIEN N (FR); PF MEDICAMENT (FR);
RAULY ISABELLE (FR); ANDREONI CHRISTINE (FR); BAUSSANT THIERRY (FR)
LOCATION/Qualifiers
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
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Sequence 1 from Patent W09949892.
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Klebsiella pneumoniae
Bacteria: Proteobacteria: Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
Bacteria: Proteobacteria: Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
Bacteria: Proteobacteria: Gammaproteobacteriales;
Bacteria: Proteobacteria: Gammaproteobacteria; Enterobacteriales;
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Use of active P40 conjugates for nasal delivery.
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        Coganism="Klebsiella pneumoniae"
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CAGCCGGCGGG 1031
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BD222264
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Best Local Similarity 99.5%;
Matches 1027; Conservative
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GenCore version 5.1.6
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- protein search, using sw model OM protein

January 19, 2005, 16:38:49; Search time 95 Seconds (without alignments) 2083.462 Million cell updates/sec Run on:

US-09-913-772-2

1823 1 MKAIFVLNAAPKDNTWYAGG......DRRVEIEVKGYKEVVTQPAG 344 Perfect score: Sequence:

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Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P24017 klebsiella	P09146 enterobacte	P02935 shigella dy	P02934 escherichia	Q6w821 shigella so	Aap74759 shigella	Q6pnm6 shigella bo	Aat02227 shigella	ø	Q8z7s0 salmonella		Q8cw76 escherichia	Q7ud17 shigella fl	Q83rx2 shigella fl	Q7x0i7 shigella fl		Q6qt47 salmonella	Aas18468 salmonell		Q8d056 yersinia pe	69 yersini		Q7n602 photorhabdu	Q9rm69 erwinia car	Q99114 escherichia	Q47880 escherichia	P24747 escherichia	Q99115 escherichia	P24754 escherichia	Q99123 enterobacte	Q99124 escherichia
SUMMARIES	QI	OMPA KLEPN	OMPA_ENTAE	OMPA_SHIDY	OMPA_ECOLI	Q6W8 <u>2</u> 1	AAP74759	Q6 PNM6	AAT02227	Q9L6J0	082750	OMPA SALTY	Q8CW76	Q7UD17	Q83RX2	Q7X017	OMPA_SERMA	Q6QT47	AAS18468	Q8ZG77	Q8D056	AAS61569	Q6D6D4	Q7N602	Q9RM69	099114	Q47880	OMPA ESCFE	Q991 <u>1</u> 5	OMPA ESCHE	099123	OMPA_ESCBL
	DB	-	٦	П	Н	7	~	~	~	~	~	ч	~	~	~	7	-	~	7	~	~	7	~	7	~	~	~	ч	~	-	~	Н
	Length	344	350	351	346	346	346	346	346	346	350	350	379	348	372	327	359	319	319	353	363	363	366	368	367	238	244	243	244	243	238	241
d	Query Match	99.5	84.6	83.7	82.9	82.9	82.9	82.7	82.7	82.6	82.2	82.0	81.6	80.8	80.8	80.4	75.8	74.8	74.8	72.7	72.7	72.7	71.6	70.7	69.3	61.9	61.0	6.09	60.9	60.7	60.1	59.7
	Score	1813	1542	1525.5	1511	1511	1511	1507	1507	1505	1499	1495	1487	1473	1473	1466	1381.5	1364	1364	1325.5	1325.5	1325.5	1306	1289	1262.5	1128.5	1112.5	1111	1110.5	1106	1095.5	1089
	Result No.	1	7	m	4	5	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24			27		29	30	31

EMBL; M63355; AAA25119.1; -. HSSP; P02934; 1QJP.
InterPro; IPR006664; Bac OmpA.
InterPro; IPR0002368; OmpĀ.
InterPro; IPR006665; OmpĀ/MotB.
InterPro; IPR006690; OMPĀ\_LIKE.

P24016 citrobacter 0916i9 salmonella 0916i9 shigella fil p24755 serratia od 06waf8 klebsiella 06waf7 klebsiella 06waf7 klebsiella 06waf7 klebsiella Aaq96090 klebsiella Aaq96090 klebsiella 06wag0 klebsiella 06wag1 klebsiella 06wag1 klebsiella 06wag1 klebsiella 06wag1 klebsiella	
OMPA_CITFR Q91.6I9 Q91.6I9 OMPA_SEROD Q6WAF8 Q6WAF7 Q6WAF7 Q6WAF7 AAQ96098 AAQ96090 AAQ96091 Q6WAG1	
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1056.5 10042	
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## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
STRAIN=RV 308;
MEDLINE=9819254; PubMed=9524233;
MEDLINE=98192544; PubMed=9524233;
MGUYEN T.N., Samuelson P., Sterky F., Merle-Poitte C., Robert A.,
MGUYEN T.N., Baquening using a PCR-based biotin-capture method
"Chromosomal sequencing using a PCR-based biotin-capture method
allowed isolation of the complete gene for the outer membrane protein
A of Klebsiella pneumoniae.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Klebsiella.
                                             P24017; 069435;
01-MAR-1992 (Rel. 21, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Outer membrane protein A precursor (Outer membrane protein II).
     344 AA
     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 93-335 FROM N.A.
STRAIN=LD119;
MEDLINE=92065252; PubMed=1955870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ000998; CAA04450.1; -.
     STANDARD;
                                                                                                                                                                                                                                                                                                                              Name=ompA;
Klebsiella pneumoniae.
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OMPA_KLEPN
     HID DAY REPAYED BY THE PROPERTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY
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   Pfam; PF00691; OmpA; 1.
Pfam; PF01691; OmpA; 1.
PRINTS; PR01021; OMFADOMAIN.
Prodom; PD000930; OmpA/MotB; 1.
PROSITE; PS01068; OMPA; 1.
Conjugation; Outer membrane; Phage recognition; Porin; Repeat; Signal; Transmembrane.
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Enterobacteriaceae; Enterobacter.
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                                                                                                                                                 Potential.
Potential.
4 X 2 AA tandem repeats of A-P.
                                                                                                                                                                                                                                                              Score 1813; DB 1; Length 344;
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Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
                                                                                                                                                                                                                                            37061 MW; AC88AAE3B7871B16 CRC64;
                                                                                    Outer membrane protein
                                                                                                                                                                                                                OmpA-like.
By similarity.
Y -> I (in Ref. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterobacter aerogenes (Aerobacter aerogenes)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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                                                                                                    Potential.
Potential.
Potential.
Potential.
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MEDLINE=84108348; PubMed=6363059;
nterPro; IPR000498; OmpA_tmem.
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P09146;
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InterPro; IPR002664; Bac_OmpA.
InterPro; IPR002669; OmpA.
InterPro; IPR006659; OmpA.
InterPro; IPR006659; OmpA_LIKE.
InterPro; IPR006699; OMPA_LIKE.
InterPro; IPR006991; OmpA_Limem.
Pfam; PF001389; OmpA_membrane; 1.
Pfam; PF01389; OmpA_membrane; 1.
PRINTS; PR01021; OMPADOMAIN.
ProDom: PD000930; OmpA/MotB; 1.
PR051TE; PS01068; OMPA; 1.
Conjugation; Outer membrane; Phage recognition; Porin; Repeat; Signal;
Braun G., Cole S.T.;
"Molecular characterization of the gene coding for major outer
membrane protein Omp4 from Enterobacter aerogenes.";
Eur. J. Biochem. 137:495-500(1983).
-!- FUNCTION: Required for the action of colicins K and L and for the
stabilization of mating aggregates in conjugation. Serves as a
receptor for a number of T-even like phages. Also acts as a porin
with low permeability that allows slow penetration of small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV
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solutes (By similarity).
-!- SUBUNIT: Monomer (Probable).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
-!- SIMILARITY: Belongs to the ompA family.

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4 X 2 AA tandem repeats of A-P.
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87.5%; Pred. No. 3e-110;
ive 10; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Figurity.
6276C6F2F21065DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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By similar
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295; Conservative
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315
350 AA;
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Best Local
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351 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-82221414; PubMed-6283478;

MEDLINE-82221414; PubMed-6283478;

MEDLINE-82221414; PubMed-6283478;

MEDLINE-82221414; PubMed-6283478;

Maraun G., Cole S.T.;

The nucleotide sequence coding for major outer membrane protein OmpA

T The nucleotide sequence for the action of colicins K and L and for the action of colicins K and L and for the action of mating aggregates in conjugation. Serves as a receptor for a number of T-even like phages. Also acts as a porin with low permeability that allows slow penetration of small solutes (By similarity).

C SUBCELULAR LOCATION: Integral membrane protein. Outer membrane.

C SIMERILUAR LOCATION: Integral membrane protein. Outer membrane.
192 SYRFGQEDNAPVVAPAAPAPAPEVTTKTFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 251
                                                                                MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT
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PRODOM; PD000930; OMPA/MotB; 1.
PROSITE; PS01068; OMPA; 1.
Conjugation; Outer membrane; Phage recognition; Porin; Repeat; Signal; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
NCBL_TaxID=622;
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Outer membrane protein A precursor (Outer membrane protein II)
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HSSP; P02934; 1QJP.
INCEPTO; IPR006664; Bac_OmpA.
InterPro; IPR006664; OmpA,
InterPro; IPR006665; OmpA/MotB.
InterPro; IPR006690; OMPA_LIKE.
InterPro; IPR000499; OmpA_LIKE.
Fam; PF00691; OmpA, 1.
Pfam; PF01389; OmpA, membrane; 1.
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Escherichia coli O157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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01-OCT-2004 (Rel. 45, Last annotation update)
Outer membrane protein A precursor (Outer membrane protein II*).
Name=ompA; Synonyms+tolg, tut, con;
OrderedLocusNames=b0957, 21307, ECS1041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILINE-810(53729, PubMed-6253901,
Beck E., Bremer E.;
Wholeotide sequence of the gene ompA coding the outer membrane protein II of Escherichia coli K-12.",
Nucleic Acids Res. 8:3011-3024(1980).
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"Gene structure of the OmpA protein, a major surface protein of
Escherichia coli required for cell-cell interaction.";
J. Mol. Biol. 143:317-328(1980).
                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                DB 1; Length 351;
4 X 2 AA tandem repeats of A-P.
                                                                                                                                                                                                                                          83.7%; Score 1525.5; DB 1; Length
84.6%; Pred. No. 5.6e-109;
ive 20; Mismatches 27; Indels
                                                                                                                                OmpA-like.
By similarity.
1499AA5F5395B35B CRC64;
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STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed=9278503;
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Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura Y., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
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receptor for a number of T-even like phages. Also acts as a porin with low permeability that allows slow penetration of small
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                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane. MASS SPECTROMETRY: MW=35177; METHOD=Electrospray; RANGE=22-346; NOTE=Ref.20.
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Enterobacteriaceae; Shigella.
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Kirmpal-Kaur B., Mohd Zaki S., Asma I., Ravichandran M.;
Kirmpal-Kaur B., Mohd Zaki S., Asma I., Ravichandran M.;
Submitted (Max-2003) to the SWBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ompA family.
EMBL, AX105874; AAP74759.1; -.
InterPro; IPR006664; Bac_OmpA.
InterPro; IPR001035; MotY.
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84.9%; Pred. No. 7.1e-108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKSN-- 130
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 346;
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                                                                                                                                                                                                                                                                                                                1 21 Potential.
346 AA; 37201 MW; 195147734CDF8B04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 21 Potential.
346 AA; 37201 MW; 195147734CDF8B04 CRC64;
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02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
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Local Similarity 84.9%; Pred. No. 7.1e-108;
Nes 286; Conservative 17; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                82.9%; Score 1511; DB 2;
84.9%; Pred. No. 7.1e-108;
ive 17; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Outer membrane protein A precursor
                                                                            Pfam; PF00691; OmpA; 1.
Pfam; PF01389; OmpA membrane; 1.
PRINTS; PR01023; NAFLGMOTY.
PRINTS; PR01021; OMPADOMAIN.
PRINTS; PR010221; OMPADOMAIN.
PLODOM; PD000930; OUTRWHBRANEA.
PROSITE; PS01068; OMPA, 1.
InterPro; IPR006665; OmpA/MotB.
InterPro; IPR006690; OMPA_LIKE.
InterPro; IPR000498; OmpA_tmem.
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Matches 286; Conservative
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248 LDPKDGSVVVLGYTDRIGSDAYNQGLSERRAQSVVDYLISKGIPVDKISARGMGESNPVT 307
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                                                                                                                               188 SYRFGOGEAADVVADADADADADADEVOTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSN
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                                                                                                                                                                                                         MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT
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                                                                                                    SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN
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STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV
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STRAIN=MalaysiasB631;
Nik Noorul Shakira M.S., Kirnpal-Kaur B.S., Ravichandran M., Asma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shigella boydii.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Shigella.
NCBI_TaxID=621,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 82.7%; Score 1507; DB 2; Length 346; Local Similarity 84.6%; Pred. No. 1.4e-107; nes 285; Conservative 17; Mismatches 25; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mohd Zaki S.;
"Shigella boydii outer membrane protein A precursor (omg
Submitted (ARR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY590298; AAT02227.1; -.
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SEQUENCE 346 AA; 37229 MW; E94650734CDF9239 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-MAY-2004 (TrEMBLrel. 27, Created)
10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
10-MAY-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                             GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
                                                                                                                                                                                                                                                                                                                                         308 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 344
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SIZURAIN=MalayaiaSB631;

Nak Noorul Shakira M.S., Kirnpal-Kaur B.S., Ravichandran M., Asma I.,
Nak Noorul Shakira M.S., Kirnpal-Kaur B.S., Ravichandran M., Asma I.,
Nah Mohd Zaki S.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.

- I- SIMILARITY: Balongs to the ompA family.

REMBL; AYS02989; AAT02227.1; -.

REMBL; AYS02989; AAT02227.1; -.

RITERPRO; IPR006664; Bac CompA.

RITERPRO; IPR006669; OmpA.

RITERPRO; IPR006669; OmpA/MorB.

InterPro; IPR00669; OmpA/MorB.

InterPro; IPR00699; OmpA/MorB.

REAM; PP001389; OmpA, 1..

REAM; PR01021; OMPADOWAIN.

PRINTS; PR01021; OMPADOWAIN.

PRINTS; PR01022; OUTRWHERANEA.

PRODOM; PD000930; OmpA/MorB; 1.

RECORD PROSOURS OMPA/MORB; 1.
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                                                                                                                                                     126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                                                                                                                                                                                   ---VYGKNHDIGVSPVFAGGVEYAITPEIATRLEYOWTNNIGDAHTIGTRPDNGMLSLGV 187
                                                                                                                                                                                                                                                            SYRFGQEDAAPUVAPAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
                                                                                                                                                                                                                                                                                        MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
                                                                                                                                                                                                                                                                                                                                                                                               EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
                                                EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
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                                                                            73 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKSN--
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18 VAQAAPKDNTWYTGAKLGWSQYHDTGFI - - - - NNNGPTHENQLGAGAFGGYQVNPYVGF
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 21 Potential.
346 AA; 37229 MW; E94650734CDF9239 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Outer membrane protein A precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 344
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84.6%; Pred. No. 1.4e-107;
iive 17; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=621;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=ompA;
                                                99
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Best Local &
                                                                                                                                                                                                      131
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SIGNAL
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Pfan; PP00691; OmpA; OmpA; Dfan; PP01389; OmpA; DraELANTS; PR01022; OmpAGDONTY. PRINTS; PR01021; ONFADOMAIN. PRINTS; PR01022; OUTRAMBRANEA. ProDom; P000930; OmpA/MotB; I. PROSITE; PS01068; OMPA; I. Complete proteome. SEQUENCE 350 AA; 37477 MM; EEB
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InterPro; IPR006665; OmpA/MotB.
InterPro; IPR006690; OMPA_LIKE.
InterPro; IPR000498; OmpA_tmem.
                                Enterobacteriaceae; Salmonella
                                                                                                                                                                                                                                                                                           Nature 413:848-852(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 279; Conserv
                                                                [1] TSEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
 Salmonella typhi
                                             NCBI_TaxID=601;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYRFGQGEAAPVVAPAPAPAPEVQTKHFTLKSDVLFTFNKATLKPEGQAALDQLYSQLSN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | MDPKDGSAVVLGYTDR1GSEAYNQQLSEKRAQSVVDYLVAKG1PAGK1SARGMGESNPVT 305
                                                                                                                                                                                                                 Wang Y., Kim K.S.;
STRAIN-MASJELS;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

1. SIMILARITY: Belongs to the ompA family.

1. SIMILARITY: Belongs to the ompA family.

REMBL; AP234269; AAP37887.1; -.

REMBL; AP234269; AAP37887.1; -.

ROS GO.006279; C:outer membrane (sensu Gram-negative Bacteria); IEA.

GO; GO.0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.

ROS GO:0005198; F:structural molecule activity; IEA.

ROS GO:0005198; F:structural molecule activity; IEA.

RITEPTO; IPR00664; Bac_OmpA.

RITEPTO; IPR006665; OmpA.

RITEPTO; IPR00669; OmpA.

RITEPTO; IPR00699; OmpA. LINE.

REAM; PF001389; OmpA. LINE.

REAM; PF01389; OMPA. LINE.

REAM; PF01389; OMPA. LINE.

REAM; PF01389; OMPA. MEMBRANEA.

READOM; PD000930; OMPAMALNEA.

READOM; PR00068; OMPA, I.

RECOURTE: PS01068; OMPA, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.6%; Score 1505; DB 2; Length 346; 84.3%; Pred. No. 2.1e-107; ive 18; Mismatches 25; IndelB 10
                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8Z7S0; Q7C962;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Outer membrane protein A.
Name-ompA; OrderedLocusNames=STY1091, t1850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNICDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 344
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346 AA
                                Created)
PRT;
                           01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2004 (TrEMBLrel. 26,
                                                                             Outer membrane protein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 284; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                             Escherichia coli.
                                                                                                                                                           NCBI_TaxID=562;
                                                                                                                                                                                                          STRAIN=RS218;
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Q9L6J0;
Q9L6J0;
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RESULT 10 Q827S0 ID Q827S AC Q827S DT 01-MA DT 01-OC DE OUTER GN NAME =

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMGYDWLGRMPYKGDNTNGAYKAQGVQLTAKLGYPITDDLDVYTRLGGMVWRADTKSNVP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Bashama D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
GO; GO:0009198; F:structural molecule activity; IEA.
InterPro; IPR006664; Bac OmpA.
InterPro; IPR001035; MotY.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                     MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 AA; 37477 MW; EEB90059DFCADFD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.2%; Score 1499; DB 2; llarity 82.8%; Pred. No. 6e-107; Conservative 26; Mismatches 26;
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                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                               TRANSMEM
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REPEAT
                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
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   252 LDPKDGSVVVLGFTDRIGSDAYNQGLSEKRAQSVVDYLISKGIPSDKISARGMGESNPVT 311
                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Outer membrane protein A precursor (Outer membrane protein 33K) (Outer membrane major heat-modifiable protein).
Name-omph? OrderedLocusNames=STM1070;
Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN=LT2 / SGSC1412 / ATCC 700720;

MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;

MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;

MCCleiland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Mauyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan B., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 413:852-856 (2001).

-!- FUNCTION: Required for the action of colicins K and L and for the stabilization of mating aggregates in conjugation. Serves as a receptor for a number of T-even like phages. Also acts as a porin with low permeability that allows slow penetration of small solutes (By similarity).
-!- SUBUNIT: Monomer (Probable).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
-!- SIMILARITY: Belongs to the ompA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO1021; OMPADOMAIN.
ProDom; PD000930; OmpA/MotB; 1.
PROSITE; PS01068; OMPA; 1.
Complete proteome; Conjugation; Outer membrane; Phage recognition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and molecular characterization of the ompA gene from Salmonella typhimurium.";
                                                                                                   312 GNTCDNVKPRAALIDCLAPDRRVEIEVKGVKDVVTQP 348
                                                               306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
                                                                                                                                                                                                                                                                                                 350 AA
                                                                                                                                                                                                                                                                                             PRT;
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Stydene; SG10263; ompA.
InterPro; IPR006664; Bac.OmpA.
InterPro; IPR006669; OmpA.
InterPro; IPR006690; OMPA LIKE.
InterPro; IPR000499; OmpA-tmem.
Pfan; PF01389; OmpA, membrane; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=83287368; PubMed=6349993;
Freudl R., Cole S.T.;
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                                                                                                                                                                                                                                                                                             STANDARD;
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P02936;
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EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 G-GPSTXDHDTGVSPVFAGGIEYAITPEIATRLEYQWTNNIGDANTIGTRPDNGLLSVGV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF
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STRAIN=06:H1 / CFT073 / ATCC 700928 / UPEC;
MEDLINE=23388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
Melch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mayhew G.F., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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9
                                                                                                                                                                                                        Potential.
4 X 2 AA tandem repeats of A-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                  By similarity.
V -> F (in Ref. 1).
S -> I (in Ref. 1).
; B4AC52C8C5DF54FB CRC64;
                                        protein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 1495; DB 1;
; Pred. No. 1.2e-106;
26; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNTCDNVKPRAALIDCLAPDRRVEIEVKGVKDVVTQP
                                        membrane
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                                                        Potential.
Potential.
Potential.
Potential.
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Potential.
Potential.
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  Transmembrane.
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Name=ompA; OrderedLocusNames=c1093;
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                                                                                                                                                                                                                                                                                                                                                                                                                37515 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.0%;
82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 82.8°
Matches 279; Conservative
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                   21
350
40
67
67
107
1126
1136
212
208
210
Signal;
                                                                                                                                                                                                                                                                                                                                                                                             247 ;
350 AA;
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CONFLICT
SEQUENCE
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Name=ompA; OrderedLocusNames=SF0957;
                                                                                                                                                                                                                                      Best Local Similarity 83.48
Matches 281; Conservative
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                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYRFGQEDAAPUVAPAPAPAPATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
                                                                                                                                                                                                                                                                                                                                                                                                             6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF 65
                                                              HSSP; P02934; IQJP.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
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MEDLINE=22590274; PubMed=12704152;
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
Wei J., Goldberg M.B., Plunkett G. III, Rose D.J., Darling A.,
Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
Schwartz D.C., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence and comparative genomics of Shigella
                                                                                                                                                                                                                                                                                                                                               Length 379;
                                                                                                                                                                                                                                                                                                                                               81.6%; Score 1487; DB 2; Length 3 83.7%; Pred. No. 5.6e-106; ive 17; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                  Complete proteome.
SEQUENCE 379 AA; 41054 MW; CE396D152EB1EDCA CRC64;
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MRX-2004 (TrEMBLrel. 26, Last annotation update)
Outer membrane protein 3a (11*,6,4).
Name-ompA, OrderedLocusNames=$1023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003 (TrEMBLrel. 25, Created) 01-OCT-2003 (TrEMBLrel. 25, Last RPM
                                                                                                                     InterPro; IPR006664; Bac OmpA.
InterPro; IPR006664; Dac OmpA.
InterPro; IPR006665; OmpA/NotB.
InterPro; IPR00690; OmpA_LIKE.
InterPro; IPR00690; OmpA_LIKE.
InterPro; IPR000498; OmpA_LIKE.
Pfam; PF00691; OmpA; 1.
PRIMTS; PR01021; OMPADOMAIN.
PRINTS; PR01022; OUTRWMBRANEA.
                                                                                                                                                                                                                                                                  ProDom; PD000930; OmpA/MotB; 1
PROSITE; PS01068; OMPA; 1.
                                                                                                                                                                                                                                                                                                                                                              Local Similarity 83.7
1es 282; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 SYRFGQEDAAPVVAPAPAPAPAFATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 SYRFGQGEAAPVV--APAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-441(2002).
-!- SIMILARITY: Belongs to the ompA family.
EMBL; AE015125; AAN42586.1; -.
HISSP; PO2934; IQJV.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF
flexneri serotype 2a strain 2457T.";
Infect. Immun. 71:2775-2786(2003).
BMBL; ARD169BL; AARD1471.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
InterPro; IPR006665; OMPA_INKE.
InterPro; IPR00699; OMPA_INKE.
InterPro; IPR000499; OMPA_INKE.
Ffam; PF00691; OmpA, membrane; 1.
Pfam; PF01389; OmpA, membrane; 1.
Propon; PB000930; OmpA, Membrane; 1.
PROSITE; PS01068; OMPA, Membrane; 1.
PROSITE; PS01068; OMPA, Membrane; 1.
SEQUENCE 348 AA; 37283 MW; 42623C67041D62F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Ran B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 SYRFGGGEAAPVV--APAPAPEVQTKHFTLKSDVLFNFRTLKPEGGAALDQLYSQLSN 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 SYRFGQEDAAPVVAPAAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=USM401,

A Mohd Zaki S., Kirnpal-Kaur B., Ravichandran M., Asma I.;

Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.

L. Submitted (OCT-2003) to the embL/GenBank/DDBJ databases.

-!- SIMILARITY: Belongs to the ompA family.

R EMBL; AY305875; AAP74760.2; -.

R GO; GO:0009289; C:flagellum (Sensu Bacteria); IEA.

R GO; GO:0009279; C:outer membrane; IEA.

R GO; GO:000379; F:motor activity; IEA.

R GO; GO:000379; F:ciliary/flagellar moitlity; IEA.

R GO; GO:0005198; F:structural molecule activity; IEA.

R GO; GO:0005198; F:structural molecule activity; IEA.

R GO; GO:0005198; F:structural molecule activity; IEA.

R GO; GO:0005198; F:structural molecule activity; IEA.

R GO; GO:0005198; F:structural molecule activity; IEA.

R InterPro: IPR001035; Motÿ.

R InterPro: IPR002368; Motÿ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----PNNGPTHENQLGAGAFGGYQVNPYVGF 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF
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Enterobacteriaceae, Shigella.
NCBI_TaxID=42897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30; Indels
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR00664; Bac OmpA.
InterPro; IPR006665; OmpA.
InterPro; IPR006665; OmpA.MotB.
InterPro; IPR006690; OmpA.LIKE.
InterPro; IPR006498; OmpA.LIKE.
InterPro; IPR006498; OmpA.LIKE.
InterPro; IPR006499; OmpA.LIKE.
InterPro; IPR00691; OmpA.I.
Pfam; PF01389; OmpA.membrane; 1.
PRINTS; PR01021; OMPA.DMAIN.
PRINTS; PR01022; OMPA.MotB; 1.
PROSITE; PS01068; OMPA.I.
IPROSITE; PS01068; OMPA.I.
IPROSITE; PS01068; OMPA.I.
COmplete profeome.
SEQUENCE 372 AA; 40289 MW; E5D55235EIFOCF1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                     372 AA; 40289 MW; E5D55235E1F0CF1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306 GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 370
                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 1473; DB 2;
; Pred. No. 6.5e-105;
18; Mismatches 30;
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Best Local Similarity 83.4%
Matches 281; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 SFKDHDIGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDANTIGTRPDNGLLSLGVSYRF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 DGSVVVLGYTDRIGSDAYNQGLSERRAQSVVDYLISKGIPADKISARGMGESNPVTGNTC 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 APKDNTWYTGAKLGWSQYHDTGFI-----PNNGPTHENQLGAGAFGGYQVNPYVGFEMGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 DWLGRMPYKGDNINGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTKANVPG-GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 SRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 GQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 DGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         8;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 80.4%; Score 1466; DB 2; Length 327; Best Local Similarity 83.8%; Pred. No. 1.9e-104; Matches 279; Conservative 18; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                      NON TER 1 1
SEQUENCE 327 AA; 35254 MW; 31AEFD69EF7A6182 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 DNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
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InterPro; IPR006665; OmpA/MotB.
InterPro; IPR006690; OMPA LIKE.
InterPro; IPR006690; OMPA LIKE.
Pran; PP00691; OmpA; 1..
Pfam; PP00691; OmpA; 1..
PRINTS; PR01023; OmpA membrane; 1.
PRINTS; PR01023; OMPADOMAIN.
PRINTS; PR01022; OUTRWMBRANEA.
PRODOM; PD000930; OMPA/MOCB; 1.
PROSITE; PS01068; OMPA/MOCB; 1.
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Search completed: January 19, 2005, 18:16:30 Job time : 100 secs

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                  Copyright
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- protein search, using sw model OM protein Run on:

January 19, 2005, 17:58:00 ; Search time 24 Seconds (without alignments) 1379:107 Million cell updates/sec

US-09-913-772-2

1 MKAIFVLNAAPKDNTWYAGG..........DRRVEIEVKGYKEVVTQPAG 344 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cription	outer membrane pro	outer membrane pro	outer membrane pro		outer membrane pro	outer membrane pro	outer membrane pro	outer membrane pro	outer membrane pro	probable outer mem	outer membrane pro	outer membrane pro		outer membrane pro	outer membrane pro	outer membrane pro	outer membrane pro	outer membrane pro	outer membrane pro	outer membrane pro	outer membrane pro	outer membrane pro	outer membrane pro	21K outer membrane	outer membrane pro	outer membrane pro	outer membrane cla	outer membrane pro	root adhesin - Pse
SUMMARIES	ΩI	JC6558	807222	MMEBAD	MMECA	A90759	G85622	AI0626	MMEBAT	807298	AD0175	162385	I62393	162388	I62389	I84531	162386	I62387	162391	162394	I40703	C64187	E84968	F82104	A45275	A27894	C81205	A37004	œ	S20494
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	Length	35.	35	35	346	34	34	32	35	35	35.	23	24,	24	24	243	243	241	241	240	238	353	34	32:	194	23(	242	240	24.	32(
940	Query Match	97.8	84.6	83.7	82.9	82.9	82.9	82.2	81.7	75.8	72.7	61.9				8.09									14.	14.	14.	13.	H	П
	Score	1782	1542	1525.5	1511	1511	1511	1499	1490	1381.5	1325.5	1128.5	1112.5	1111	1110.5	1109	1106	1089	1084	1074.5	1056.5	646.5	515	443.5	271	262	255	251	250	243
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RESULT S07222

outer membrane pro	OmpA family protei	outer membrane fib	outer membrane pro	outer membrane pro	probable outer mem	OmpA family protei	hypothetical 22.2K	probable outer mem	probable outer mem	probable outer mem	probable outer mem	probable ompA prot	probable membrane	probable lipoprote	hypothetical prote
839156	H87341	C81294	A39139	B82819	A83516	D87682	847773	E83185	AC0982	E91183	A86030	H70782	H95302	C82230	A83541
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12.7 350 2	407 2	319 2				-							•		
	12.5 407 2	11.4 319 2	11,3	11.3	10.9	10.6	8.6	6.7	7.6	9.5	9.5	9.5	4.6	9.3	9.3

## ALIGNMENTS

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C,Accession: UC6558
R;Nguyen, T.N.; Samuelson, P.; Sterky, F.; Merle-Poitte, C.; Robert, A.; Baussant, T.; H
Gene 210, 93-101, 1998
A;Title: Chromosomal sequencing using a PCR-based biotin-capture method allowed isolatio
A;Reference number: UC6558; MUID:98192544; PMID:9524233
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-356 <NGU>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 SYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77
                                      outer membrane protein A precursor - Klebsiella pneumoniae
C;Species: Klebsiella pneumoniae
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYRFGGEDAAPVVAPAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGGQALDQLYTQLSN
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0
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C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-356/Product: outer membrane protein A #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 97.8%; Score 1782; DB 2; Length 356; Best Local Similarity 99.4%; Pred. No. 4.1e-127; Matches 336; Conservative 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPA 343
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DB 1; Length 351;

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F;214-351/Domain: periplasmic #status predicted <PER>
                                                                                  Local Similarity
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outer membrane protein ompA precursor - Enterobacter aerogenes
C;Species: Enterobacter aerogenes
C;Species: Enterobacter aerogenes
C;Apecies: Enterobacter aerogenes
C;Apecies: Enterobacter aerogenes
C;Apecies: Enterobacter aerogenes
C;Apecies: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: 807222
Br. J. Biochem: 137, 495-500, 1983
A;Title: Molecular Characterization of the gene coding for major outer membrane protein
A;Reference number: 807222; MUID:84108348; PMID:6363059
A;Accession: 807222
A;Accession: 807222
A;Accession: 807222
A;Accession: 807222
A;Accession: 807222
A;Accession: 807222
A;Accession: 807222
A;Accession: 807222
A;Accession: 807222
A;Accession: Bandon Canalated the codon CAG for residue 197 as Asn
C;Genetics:
A;Accession: 80mpA
C;Genetics:
A;Accession: 80mpA
C;Accession: 80mpA
E;22-350/Product: outer membrane protein ompA #status predicted cPER>
F;22-350/Product: outer membrane protein ompA #status predicted cPER>
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C;Genetics:
A;Gene: ompA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNSIAGDNHDIGVSPVFAGGVEWAMTRDIATRLEYQWVNNIGDAGTVGVRPDNGMLSVGV 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
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Outer membrane protein A precursor - Shigella dysenteriae
Outer membrane protein A precursor - Shigella dysenteriae
Cispecies: Shigella dysenteriae
Cispecies: Shigella dysenteriae
Cispecies: Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
Cispecies: And 35
Ribraun, G.; Cole, S.T.
Nucleic Acids Res. 10, 2367-2378, 1982
A;Title: The nucleotide sequence coding for major outer membrane protein Omp A;Teference number: A03435; MUID:82221414; PMID:6283478
A;Accession: A03435
A;Molecule type: DNA
A;Residues: 1-351 - BRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF
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C,Keywords: transmembrane protein
F,1-21/Domain: signal sequence #status predicted <SIG>
F,22-351/Product: outer membrane protein A #status predicted <MAT>
F,22-201/Domain: intramembrane #status predicted <INT>
F,22-201/Region: alanine/proline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26; Indels
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%; Pred. No. 5.4e-109;
10; Mismatches 26;
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87.5%;
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Best Local Similarity 87.5%
Matches 295; Conservative
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A, Experimental source: strain K12
R, Movva, N. R., Nakamura, K.; Inouye, M.
J. Mol. Biol. 143, 317-328, 1980
A, Title: Gene structure of the OmpA protein, a major surface protein of Escherichia coli
A, Reference number: A92862, MUID:81170587; PMID:6260961
A, Reference number: A92862
A, Accession: A92862
A, Molecula type: DNA
A, Residues: 1-346 < MOV>
A, Cross-references: GB:J01654; GB:V00307; GB:V00358; NID:g146979; PIDN:AAA24231.1; PID:g1
A, Escharimental source: K12, strain K802
A, Experimental source: K12, strain K802
B, Chen, R.; Schmidmayr, W.; Kramer, C.; Chen-Schmeisser, U.; Henning, U.
Proc. Natl. Acad. Sci. U.S.A. 77, 4592-4596, 1980
A, Title: Primary structure of major outer membrane protein II* (ompA protein) of Escheric A, Reference number: A93855; MUID:81054820; PMID:7001461
A, Molecula type: protein
A, Molecula type: Drotein
A, Residues: 22-346 < CHE>
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R;Kuhn, A.; Kiefer, D.; Koehne, C.; Zhu, H.Y.; Tschantz, W.R.; Dalbey, R.B.
Bur. J. Biochem. 226, 891-897, 1994
Aj:Title: Evidence for a loop-like insertion mechanism of pro-Omp A into the inner membrar A;Reference number: $50909; MUID:95112855; PMID:7813480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: protein
A,Residues: 1-46 <KUH>
R,Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EBC
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A;Residues: 1-346 <BEC>
A;Cross-references: UNIPROT:P02934; GB:V00307; GB:J01654; NID:g42159; PIDN:CAA23588.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          οĘ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Outer membrane protein A precursor - Bscherichia coli (strain K-12)
N;Alternate names: outer membrane protein II*
C;Species: Bscherithia coli
C;Dspecies: Bscherithia coli
C;Date: 30-Sep-1980 #text_change 09-Jul-2004
C;Accession: A93707; A92862; A93855; S50909; D64836; A03434
R;Beck, E; Bremer, E
Nucleic Acids Res. 8, 3011-3024, 1980
A;Title: Nucleotide sequence of the gene ompA coding the outer membrane protein II
A;Reference number: A93707; MUID:81053729; PMID:6253901
                                                                                                                                                                                                                                                                                                                                                              73 EMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDVYTRLGGMVWRADTKAHIN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 SYRFGGGEAAPVVAPAPAPAPEVQTKHFTLKSDVLFNFNKATLKPEGQAALDQLYSQLSN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYRFGQEDAAPVVAPAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
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                                                                                                                                                                                                                                                                                                                 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
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                                                                                                                                                                                                                                18 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----DNNGPTHENOLGAGAFGGYQVNPYVGF
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                                                                                                                                                              6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF
                                                                                 Gaps
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                                                                                 Indels
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83.7%; Score 1525.5; DB 1;
84.6%; Pred. No. 9.5e-108;
ive 20; Mismatches 27;
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A; Status: preliminary
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C; Superfamily: outer membrane protein A
                                                                                                                      Conservative
                                                                                          Similarity
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                                                                                                                   Matches 286;
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                                                                 Query Match
Best Local
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A: Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: D64836
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-346 < BLAT>
A; Croserion: DNA
A; Residues: 1-346 < BLAT>
A; Croserimental source: Strain K-12, substrain MG1655
C; Genetics: A; Genetics: Strain K-12, substrain MG1655
C; Genetics: DNA
A; Resperimental source: strain K-12, substrain MG1655
C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: C; Genetics: C; Corporation: required for the action of various solutes
C; Function: A; Map position: 2 min
C; Function: A; Map position: Equired for the action of various solutes
C; Superfamily: outer membrane protein A
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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Outer membrane protein 3a ECs1041 [imported] - Escherichia coli (strain O157:H7, sub)

CiSpecies: Escherichia coli
CiSpecies: Bscherichia coli
CiSpecies: Bscherichia coli
CiSpecies: Bscherichia coli
CiSpecies: Bscherichia coli
CiSpecies: Bscherichia coli
CiSpecies: Ascession: A90759

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, ONA Res. 8, 11-22, 2001

A;Hayashi, T.; Maunaga, T.; Kuhara, S.; Shiba, T.; Hattcri, M.; Shinagawa, H.
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and call A;Reference number: A99629; MUID:21156231; PMID:11258796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---VYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGTRPDNGMLSLGV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 82.9
Best Local Similarity 84.9
Matches 286; Conservative
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A,Molecule type: DNA
A,Residues: 1-346 <HAY>
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outer membrane protein 3a [imported] - Escherichia coli (strain O157:H7, substrain EDL93 C; Species: Escherichia coli (cjate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C; Accession: G85622 R; Perna, N.T.: Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
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A;Cross-references: UNIPROT:P02934; GB:AE005174; NID:g12514142; PIDN:AAG55443.1; GSPDB:G
A;Experimental source: strain 0157:H7, substrain EDL933
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                                                                                                                                              18 VAQAAPKDNTWYTGAKLGWSQXHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 LDPKDGSVVVLGYTDRIGSDAYNQGLSERRAQSVVDYLISKGIPADKISARGMGESNPVT
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                                                                                                                 6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF
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A;Reference number: A85480; MUID:21074935; PMID:11206551
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  Length 346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP 342
82.9%; Score 1511; DB 2; 84.9%; Pred. No. 1.2e-106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.9%; Score 1511; DB 2;
llarity 84.9%; Pred. No. 1.2e-106;
Conservative 17; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Gene: ompA
C,Superfamily: outer membrane protein A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
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Gaps

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C;Species: Serratia marcescens
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Braum, G:; Cole, S.T.
Mol. Gen. Genet. 195, 321-328, 1984
A;Title: DNA sequence analysis of the Serratia marcescens ompA gene: implications for the A;Reference number: S07298; MUID:85035845; PMID:6092858
A;Reference number: S07298
A;Molecule type: DNA
A;Residues: 1-359 <BRA>
A;Coss-references: UNIPROT:P04845; EMBL:X00618; NID:947242; PIDN:CAA25254.1; PID:g758300
                      A;Cross-references: UNIPROT:P02936; GB:X02006; NID:g47798; PIDN:CAA26037.1; PID:g758341
C;Genetics:
                                                                                                             A years: output

A, wap position: 20 min

C, Function:
A, bescription: required for the action of colicins and for the stabilization of mating in the scannot serve as the receptor for the ompA-specific phages K3 and Tull
C, Superfamily: outer membrane protein
A, Note: cannot serve as the receptor for the ompA-specific phages K3 and Tull
C, Superfamily: outer membrane protein
F, 1-21/Domain: signal sequence #status predicted <NG>
F, 2-350/Product: outer membrane protein A #status predicted <NAT>
F, 22-350/Domain: intramembrane #status predicted <INT>
F, 20-20/Domain: paraina(Pproline-rich
F, 213-350/Domain: periplasmic #status predicted <PR>
F, 213-350/Domain: periplasmic #status predicted <PR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGWVWRADSKGNYA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 G-GPSTKDHDTGVSPVFAGGIEYAITPEIATRLEYQWTNNIGDANTIGTRPDNGLLSVGV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 SYRFGQEDAAPVVAPAAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192 SYRFGQOEAAPVVAPAPAPAPEVQTKHFTLKSDVLFNFNKSTLKPEGQQALDQLY1QLSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <MAT>
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(S. Superfamily: outer membrane protein A
(S. Superfamily: outer membrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;2-2-30/Product: outer membrane protein ompA #status predicted
F;22-209/Domain: intramembrane #status predicted <INI>
F;220-219/Region: alanine/proline-rich
F;220-359/Domain: periplasmic #status predicted <PER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       outer membrane protein ompA precursor - Serratia marcescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 GNTCDNVKPRAALIDCLAPDRRVEIEVKGVKDVVTOP 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 81.7%; Score 1490; DB 1; 1
Best Local Similarity 82.8%; Pred. No. 4.5e-105;
Matches 279; Conservative 24; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP
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      A;Residues: 1-350 <FRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306
                                                                                          A; Gene: ompA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
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                                                                                                                                                                                                                                       RESULT 7
A10626
outering by STY1091 [imported] - Salmonella enterica subsp. enterica serova
C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: A10626
R;Parkhill, J:; Dougan, G:; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J:; Churcher, th, T.; Connetron, P.; Cronin, A.; Davis, R.M.; Dowd, L.; White, N.; Farrar,
S:; Moule, S:; O'Gaora, P.
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: A80502; MUID:21534947; PMID:11677608
A;Recession: A10626
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-350 - PARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       outer membrane protein A precursor - Salmonella typhimurium
NyAlternate names: outer membrane major heat-modifiable protein; outer membrane protein
Sispediaes: Salmonella typhimurium
Sispediaes: Salmonella typhimurium
Cipate: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004
CyAccession: A03436
Firedul, R.; Cole, S.T.
Eur. J. Biochem. 134, 497-502, 1983
A;Title: Cloning and molecular characterization of the ompA gene from Salmonella typhimu
A;Reference number: A03436; MUID:83287368; PMID:6349993
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AL513382; PIDN:CAD08196.1; PID:g16502245; GSPDB:GN00176
C;Genetics:
A;Gene: STY1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYRFGQEDAAPWAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MDPKDGSAVVLGYTDRIGSBAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 305
EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMGYDWLGRMPYKGDNTNGAYKAQGVQLTAKLGYPITDDLDVYTRLGGMVWRADTKSNVP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252 IDPKDGSVVVLGFTDRIGSDAYNQGLSEKRAQSVVDYLISKGIPSDKISARGMGESNPVT 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Indels
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                                                                                                342
                                                                                                                                GNTCDNVKQRAALIDCLAPDRRVEIEVKGIKDVVTQP 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.2%; Score 1499; DB 2; 82.8%; Pred. No. 9.5e-106;
                                                                                                GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: outer membrane protein A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 82.89
Matches 279; Conservative
                                                                                                                                                          308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306
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                                248
                                                                                             306
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A;Cross-references: UNIPROT:047880; GB:M63350; NID:g147000; PIDN:AAA24241.1; PID:g147001
A;Experimental source: ATCC 33822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 EKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEV 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Outer membrane protein ompA - Bscherichia vulneris (ATCC 33822) (fragment)
NiAlternate names: outer membrane protein II
C;Species: Escherichia vulneris
A;Variety: ATCC 33822
A;Variety: ATCC 33822
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: I62293
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A;Title: Molecular and evolutionary relationships among enteric bacteria.
A;Atcession: I62393
A;Accession: I62393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEQYNQKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LIAKLGYPITDDLDIYTRLGGMVWRADS----SNSIAGDNHDTGVSPVFAGGVEWAMTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 DIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPEVATKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 FTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 LTAKLGYPITDDLDIYTRLGGMVWRADSKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1128.5; DB 2;
Pred. No. 5.6e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-244 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: membrane protein
F;104-115/Region: alanine/proline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 219; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable outer membrane porin A protein ompA [imported] - Yersinia pestis (strain C092)
C;Species: Yersinia pestis
C;Date: O'Svezishia pestis
C;Date: O'Svezishia pestis
C;Date: O'Svezishia pestis
C;Date: O'Svezishia pestis
C;Date: O'Svezishia pestis
C;Date: O'Svezishia pestis
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Taraga, A.M.; Chillingworth, T; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
II, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Teference number: AB00175
A;Stetus: preliminary
A;Molecule type: DNA
A;Residues: 1-533 <KUR>
A;Graus references: UNIPROT:Q8ZG77; GB:AL590842; PIDN:CAC90263.1; PID:g15979482; GSPDB:GCGGnetics:
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                                                                                                                                                                                         YASTGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSL 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNP 303
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                                                                                                           18 VAQAAPKDNTWYTGAKLGWSQYHDTGFYGNGYQNGIGNGPTHKDQLGAGAFLGYQANQYL
                                                                                                                                                                                                                                                                                                  GVSYRFGQED-AAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 AVTGNTCGYKSGRATKAQIVCLAPDRRVEIEVKGIKDVVTQPQG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVTGNTCDNVKARA--ALIDCLAPDRRVEIEVKGYKEVVTQPAG 344
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Firawrence, J.G.; Ochman, H.; Hartl, D.L.
J. Gen. Microbiol. 137, 1911-1921, 1991
A; Tetle: Molecular and evolutionary relationships among enteric bacteria.
A;Reference number: 140701; MUID:92065252; PMID:1955870
A;Reference number: ranslated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Residues: 1-244 cRBS>
A;Cross-references: UNIPROT:Q99115; GB:M63349; NID:g146992; PIDN:AAA24237.1; PID:g146993
A;Experimental source: ATCC 33821
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Moelecule: 1.-243 cRES>
A,Cross-references: UNIPROT:P24747; GB:M63351; NID:g146982; PIDN:AAA24232.1; PID:g146983
181 ERRAQSVVDYLISKGIPADKISARGMGESNPVTGNTCDNVKQRAALIDCLAPDRRVEIEV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 DIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYRFG-QEDAAPVVAPAPAPAPAVATK 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DIATRIERYQWVNNIGDAKTLGTRQDNGMLSVGVSYRFGQQEDVAPVVAPAPAPAPQVSTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272 SEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIE 331
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A;Variety: ATCC 35469
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004 C;Accession: 184531
R;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
B;Lawrence, J.G.; Ochman, H.; Hartl, D.L.
A;Title: Molecular and evolutionary relationships among enteric bacteria.
A;Fitle: Molecular and evolutionary relationships among enteric bacteria.
                                                                                                                                                                                                                                                           outer membrane protein ompA - Escherichia vulneris (ATCC 33821) (fragment) N;Alternate names: outer membrane protein II C;Species: Escherichia vulneris A;Variety: ATCC 33821 C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004 C;Accession: 162389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene: ompA
Superfamily: outer membrane protein A
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241 KG 242
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Outer membrane protein II

C,Species: Escherichia fergusonii

A,Variety: ATCC 35472

C,Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004

C,Accession: 162388; 162392

C,Accession: 162388; 162392

A,Fills: Molecular and evolutionary relationships among enteric bacteria.

A,Reference number: 140701; MUID:92065252; PMID:195870

A,Recession: 162388

A,Recession: 162388

A,Residues: Dreliminary; translated from GB/EMBL/DDBJ

A,Residues: Dreliminary; translated from GB/EMBL/DDBJ

A,Residues: Dreliminary; translated from GB/EMBL/DDBJ

A,Residues: Dreliminary; translated from GB/EMBL/DDBJ

A,Residues: Dreliminary; translated from GB/EMBL/DDBJ

A,Residues: Dreliminary; translated from GB/EMBL/DDBJ

A,Residues: 1-243 - KRES

A,Status: preliminary; translated from GB/EMBL/DDBJ

A,Residues: 1-243 - KRES

A,Status: Dreliminary; translated from GB/EMBL/DDBJ

A,Residues: 1-243 - KRES

A,Status: Dreliminary; translated from GB/EMBL/DDBJ

A,Residues: 1-243 - KRES

A,Status: Dreliminary; translated from GB/EMBL/DDBJ

A,Residues: 1-243 - KRES

A,Status: Dreliminary; translated from GB/EMBL/DDBJ

A,Residues: 1-243 - KRES

A,Status: Dreliminary; translated from GB/EMBL/DDBJ

A,Residues: 1-243 - KRES

A,Status: Dreliminary; translated from GB/EMBL/DDBJ

A,Residues: 1-243 - KRES

A,Status: Dreliminary; translated from GB/EMBL/DDBJ

A,Residues: 1-243 - KRES

A,Status: Dreliminary; translated from GB/EMBL/DDBJ

A,Residues: 1-243 - KRES

A,Status: Dreliminary; translated from GB/EMBL/DDBJ

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A,Status: Dreliminary; translated from GB/EMBL/DDBJ

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A,Status: Dreliminary; translated from GB/EMBL/DDBJ

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A,Status: Dreliminary; translated from GB/EMBL/DBJ

A,Residues: 1-243 - KRES

A,Status: Dreliminary; translated from GB/EMBL/DBJ

A,Residues: 1-243 - KRES

A,Status: Dreliminary; translated from GB/EMBL/DBJ

A,Residues: 1-243 - KRES

A,Status: Dreliminary; translated from G
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                                                                                                                       93 LTAKLGYPITDDLDIYTRLGGMVWRADSKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTR 152
                                                                                                                                                                                                                                                                              61 DIATRLEYQWYNNIGDAKTLGTRQDNGMLSVGVSYRFGQQEDVAPVVAPAPAPAPQVSTK 120
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         DB 2; Length 244;
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                                                              Indels
   Query Match 61.0%; Score 1112.5; DB 2; Best Local Similarity 87.2%; Pred. No. 9.3e-77; Matches 212; Conservative 15; Mismatches 15;
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87.2%; Pred. No. 1.2e-76;
iive 13; Mismatches 18;
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1es 211; Conservative
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93 LTAKLGYPITDDLDIYTRLGGMVWRADSKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTR 152
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                                                                 Query Match 60.8%; Score 1109; DB 2; Length 243; Best Local Similarity 87.2%; Pred. No. 1.7e-76; Matches 211; Conservative 13; Mismatches 18; Indels
A;Experimental source: ATCC 35469
C;Genetics:
A;Gene: ompA
C;Superfamily: outer membrane protein A
C;Keywords: membrane protein
F;103-114/Region: alanine/proline-rich
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Search completed: January 19, 2005, 18:16:59 Job time: 27 secs

241 KG 242

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January 19, 2005, 18:16:43; Search time 526 Seconds (without alignments) 236.281 Million cell updates/sec
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1823
1 MKAIFVLNAAPKDNTWYAGG......DRRVEIEVKGYKEVVTQPAG 344
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT7 NWW PUBL.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES		
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description	
-	1823	100.0	344	14	US-10-169-953-2	Sequence 2, Appli	
7	1511	82.9	346	16	US-10-467-421-90	Sequence 90, Appl	
m	1511	82.9	346	16	US-10-467-421-97	Sequence 97, Appl	
4	754	41.4	190	16	US-10-416-708A-24	Sequence 24, Appl	
ß	754	41.4	192	16	US-10-416-708A-27	27,	
9	748	41.0	194	16	US-10-416-708A-10	Sequence 10, Appl	
7	748	41.0	194	16	US-10-416-708A-64	Sequence 64, Appl	
80	689	37.8	344	14	US-10-336-840-9	Sequence 9, Appli	
6	688	37.7	344	14	US-10-336-840-6	Sequence 6, Appli	
10	687	37.7	137	15	US-10-432-056-2	Sequence 2, Appli	
11	687	37.7	153	σ	US-09-905-176-22	~	
12	685	37.6	344	14	US-10-336-840-3		
13	684	37.5	344	14	US-10-336-840-1	Sequence 1, Appli	

Sequence 2. Appli	4	7,	10	'n	ω	11	12	15.	15	θ,	21,	6	15	153	37,	_	m	o	Seguence 96, Appl	o	ω	oı	o,	_	ш,	۲,	w	123	7	128	12	
US-10-336-840-2	US-10-336-840-4	-10-336-840-	US-10-336-840-10		-10-336-	-10-336-	-10-336-	-09-809-665A-1	-10-854-299-15	-10-770-824	-10-467-	US-10-203-942-9	US-09-809-665A-153	US-10-854-299-153	-840 - 3	-10-770-824-1	-10-336-840-3	-10 - 467	-10-467-421-9	US-10-467-534-99	US-10-467-421-8	-10-467	-10-467-	-10-406-	-10-389-647	-10-283	US-10-282-122A-69451	US-10-323-069A-123	US-10-080-113-2	US-10-323-069A-128	US-10-323-069A-120	
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## ALIGNMENTS

RESULT 1	
Sequence 2, A publication N	-10-18-5-53-5. Sequence 2, Application US/10169953 Publication No. US20030044915A1
; GENERAL INFC ; APPLICANT:	GENERAL INFORMATION: APPLICANT: Thierry BAUSSANT
APPLICANT:	
, APPLICANT:	
; APPLICANT: ; TITLE OF I	APPLICANT: Jean-Yves BONNEFOY TITLE OF INVENTION: METHOD FOR PREPARING A POLYPEPTIDE SOLUBLE IN AN AQUEOUS SOLVENT
, TITLE C	TITLE OF INVENTION: IN THE ABSENCE OF DETERGENT
; CURRENT	FILE REFERENCE: 119390 CURRENT APPLICATION NUMBER: US/10/169,953
, CURRENT	CURRENT FILING DATE: 2002-07-03
, PRIOR A	PRIOR APPLICATION NUMBER: FR 00 00070
NUMBER	TRACK THINGS TO THE SECOND TO
; SOFTWAR	SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2	1000
TVDE DET	LENGIH: 344 TVDF: DRT
ORGANI	Artini Klebsiella pneumoniae Organism:
; FEATURE:	IB:
; OTHER INFORU US-10-169-953-2	OTHER INFORMATION: P40 0-169-953-2
Query Match	100.0%;
Best Loc Matches	Best Local Similarity 100.0%; Pred. No. 3e-160; Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
δλ	1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
qq	
ò	61 PYLGFEMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADS 120

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                                                                     KGNYASTGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGM 180
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EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
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                                                                                                                                     LSLGVSYRFGQEDAAPVVAPAPAPAPAPAFKHFTLKSDVLFNFNKATLKPEGQQALDQLY
                                                                                                                                                                                                KGNYASTGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGM
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APPLICANT: Berthet, Francois-Xavier Jacques
APPLICANT: Denoel, Philippe
APPLICANT: New, Cecile Anne
APPLICANT: Neyt, Cecile Anne
APPLICANT: Poolman, Jan
APPLICANT: Thomard, Joelle
ITLE REFERENCE: 845259
CURRENT APPLICATION NUMBER: US/10/467, 421
CURRENT APPLICATION NUMBER: US/10/467, 421
CURRENT FILING DATE: 2003-08-08
PRIOR PAPLICATION NUMBER: GB 0103171.5
PRIOR PILING DATE: 2002-02-08
PRIOR PILING DATE: 2002-03-08
NUMBER OF SEQ ID NOS: 98
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 90
                                                                                                                                                                                                                                                                                                                                                         ; Sequence 90, Application US/10467421; Publication No. US20040116665A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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US-10-467-421-90
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US-10-467-421-90
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TYPE: PRT
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US-10-416-708A-24

Sequence 24, Application US/10416708A

Sequence 24, Application US/10416708A

Sequence 24, Application US/0040161753A1

Sequence 24, Application US.0040161753A1

Seguence 24, Application Wo. US20040161753A1

APPLICANT: Wise, John G.

TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING

TITLE OF INVENTION: SPECIFICITIES

FILE REPERBENCE: 37779-0004

CURRENT PILING DATE: 2004-01-28

NUMBER OF SEQ ID NOS: 89

SOFUTANTE: Patentin version 3.2

SEQ ID NO 24

LENGTH: 190
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84.9%; Pred. No. 2.6e-131;
iive 17; Mismatches 24;
Sequence 97, Application US/10467421

Publication No. US20040116665A1

GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Berchet, Francois-Xavier Jacques
APPLICANT:
Poolman, Jan
APPLICANT:
Poolman, Jan
APPLICANT:
TILE OF INVENTION: Vaccine Composition
FILE REFERENCE: B45.25
CURRENT APPLICATION: Vaccine Composition
FILE REPERENCE: B45.25
CURRENT APPLICATION NUMBER: US/10/467,421
CURRENT FILING DATE: 2003-008
FRIOR APPLICATION NUMBER: PCT/EP02/01361
PRIOR APPLICATION NUMBER: GB 0103171.5
PRIOR FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 98
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 97
LENGTH: 346
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Best Local Similarity 84.9
Matches 286; Conservative
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ORGANISM: E.coli
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; Sequence 9, Application US/10336840; Publication No. US20030219454A1; GENERAL INFORMATION: APPLICANT: TERRY, TAMSIN DEBORAH
    NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
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                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                               Best Local Similarity 79.8
Matches 138; Conservative
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Matches 138; Conservative
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Publication No. US20040161753A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wise, John G.
APPLICANT: Fromknecht, Katja
TITLE OF INVENTION: SPECIFICITIES
FILE REFERENCE: 37779-0004
CURRENT APPLICATION NUMBER: US/10/416,708A
CURRENT FILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-416-708A-10
Sequence 10, Application US/10416708A
Sequence 10, Application US/10416708A
PUBLICALION NO. US20040161753A1
SERNEAL INFORMATION:
APPLICANT: Wise, John G.
TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING
TITLE OF INVENTION: SPECIFICITIES
FILE REFERENCE: 37779-0004
CURRENT APPLICATION NUMBER: US/10/416,708A
                                                                                                                                                                                                                                                                                           66 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125
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                                                                                                                                                                                                                  20 VAQAAPKDNIWYTGAKLGWSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVGF 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 VAQAAPKDNTWYTGAKLGWSQYHDTGFI-----NNNGPTHENQLGAGAFGGYQVNPYVGF 74
                                                                                                                                                                                      6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF
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                                                                                                                                                                                                                                                                                                                                                                             ---VYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGTRPDNG 183
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                                                                                                     Score 754; DB 16; Length 190;
Pred. No. 1.7e-61;
9; Mismatches 16; Indels 10
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Pred. No. 1.7e-61;
9; Mismatches 16;
                                        ; OTHER INFORMATION: Synthetic Construct
US-10-416-708A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Synthetic Construct US-10-416-708A-27
ORGANISM: Artificial Sequence FEATURE:
                                                                                                     Query Match
Best Local Similarity 79.9%;
Matches 139; Conservative
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Best Local Similarity 79.9%;
Matches 139; Conservative
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Sequence 64, Application US/10416708A

Sequence 64, Application US/2040161753A1

Seneral INFORMATION:
GENERAL INFORMATION:
APPLICANT:
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SEQUENCE OF INVENTION:
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                                                                                                                                                                                                  41.0%; Score 748; DB 16;
79.8%; Pred. No. 6.4e-61;
iive 9; Mismatches 16;
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) OTHER INFORMATION: Synthetic Construct US-10-416-708A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic Construct
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Query Match

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Sequence 2, Application US/10432056

Publication No. US20040014661A1

GENERAL INFORMATION:
APPLICANT: GOETSCH, Liliane
APPLICANT: HAEUW, Jean-Francois
APPLICANT: HAEUW, Jean-Francois
APPLICANT: HAEUW, Jean-Francois
APPLICANT: ROBERT, Alain
TITLE OF INVENTION: PERIPLASMIC DOMAIN OF AN ENTEROBACTERIUM OMP PROTEIN
TITLE OF INVENTION: AND ITS USE AS CARRIER OR ADJUVANT
TITLE OF INVENTION: AND ITS USE AS CARRIER OR ADJUVANT
CURRENT APPLICATION NUMBER: US/10/432,056
CURRENT FILING DATE: 2003-11-16
PRIOR FILING DATE: 2000-11-17

NUMBER OF SEQ ID NOS: 6
SEQ ID NOS: 6
SEQ ID NO 2
SEQ ID NO 2
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                                                                                                                                                61 PYLGFEMGYDWLGRMAYK-GSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRAD 119
                                                                                                                                                                              72 DNFAVELGYDDFGRAKRRQGGETVIKYTNHGAHLSLKASYPVLEGLDVYARVGAALIRSD 131
                                                                                                                                                                                                                                               120 SKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTR--DIATRLEYQWVNNIG----DAGTVG 173
                                                                                                                                                                                                                                                                                          132 YKPTKRAAPNOTHEHSLKVSPVFÄGGLEYNLPSLPELALRVEYQWVNKVGRVEKDGSRVD 191
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                                                      1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVN 60
                                                                                                   71
                                                                                                                                                                                                                                                                                                                                                                       13 LTAASVAQAAPQANTFYAGAKAGWASFHDGLNQFENSQNADGTLRN-SVTYGVFGGYQIT
                                                                                                                                                                                                                                                                                                                                           174 TRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                             234 QALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKI
         18; Gaps
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         46; Mismatches 124; Indels
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100.0%; Pred. No. 1.8e-55;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Klebsiella pneumoniae
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         153; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 QALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKI 293
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APPLICANT: TERRY, HSING-JU
APPLICANT: TERG, HSING-JU
APPLICANT: HOBB, RHONDA IVY
APPLICANT: JENNINGS, MICHAEL PAUL
APPLICANT: DOWNES, JOHN
TITLE OF INVENTION: HAEWAGGLUTININ ANTIGEN
FILE REFERENCE: 37955-0007
CURRENT APPLICATION NUMBER: US/10/336,840
CURRENT FILING DATE: 2003-01-06
PRIOR PILICATION NUMBER: PCT/AU01/00822
PRIOR PILICATION DATE: 2001-07-06
NUMBER: OF SEQ ID NOS: 39
APPLICANT: TSENG, HSING-JU
APPLICANT: HOBB, RHONDA IVY
APPLICANT: HOBB, RHONDA IVY
APPLICANT: JENNINGS, MICHAEL PAUL
APPLICANT: DOWNES, JOHN
TITLE OF INVENTION: HAEMAGGLUTININ ANTIGEN
FILE REFERENCE: 37955-0007
CURRENT RAPLICATION NUMBER: US/10/336,840
CURRENT PILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: PCT/AU01/00822
PRIOR FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 39
SCOTTWARE: PATENTIN Ver. 2.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZENGTH: 344
TYPE: PRT
ORGANISM: Haemophilus paragallinarum
                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Haemophilus paragallinarum
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SEQ ID NO 6
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es 153; Conserv
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Best Local Similarity
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US-10-336-840-6
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173
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  132 YKPTKRAAPNQTHEHSLKVSPVFAGGLEYNLPSLPELALRVEYQWVNKVGRVEKDGSRVD 191
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                                                      174 TRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1, Application US/10336840; Publication No. US20030219454A1; GENERAL INFORMATION: APPLICANT: TERRY, TAMSIN DEBORAH; APPLICANT: TSENG, HSING-JU; APPLICANT: JENNINGS, MICHAEL PAUL; APPLICANT: DOWNES, JOHN
; APPLICANT: DOWNES, JOHN
; APPLICANT: ADMINGS, MICHAEL PAUL; APPLICANT: APPLICANT: DOWNES, JOHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 37955-0007
CURRENT APPLICATION NUMBER: US/10/336,840
CURRENT FILING DATE: 2003-01-06
PRIOR APPLICATION NUMBER: PCT/AU01/00822
PRIOR FILING DATE: 2001-07-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Haemophilus paragallinarum
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Best Local Similarity 44.6*
Matches 152; Conservative
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US-10-336-840-1
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                APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
APPLICANT: Debe, Derek A.
TITLE OF INVENTION: METHOD NETHOD FROTEIN STRUCTURE FROM F
TITLE OF INVENTION: PROTEIN SEQUENCE
FILE REFERENCE: 265/297
CURRENT APPLICATION NUMBER: US/09/905,176
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US 60/218,016
PRIOR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YHDTGLI-----NNNGPTHENKLGAGAFGGYQVNPYVGFEMGYDWLGRMPYKGSVENGAY 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 153;
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44.9%; Pred. No. 1e-54;
ive 46; Mismatches 124; Indels
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APPLICANT: TERRY, HANDA JUY
APPLICANT: HOBB, RHONDA JUY
APPLICANT: JENNINGS, MICHAEL PAUL
APPLICANT: JENNINGS, MICHAEL PAUL
APPLICANT: HOBB, RHONDA JUY
APPLICANT: JENNINGS, JOHN
TITLE OF INVENTION: HAEMAGGLUTININ ANTIGEN
FILE REPERENCE: 37955-0007
CURRENT APPLICATION NUMBER: US/10/336,840
CURRENT PILING DATE: 2003-01-06
PRIOR FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PALENTIN VUMBER: PCT/AU01/00822
NUMBER OF SEQ ID NOS: 39
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; ORGANISM: Haemophilus paragallinarum
US-10-336-840-3
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                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Escherichia coli
US-09-905-176-22
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Best Local Similarity
SENERAL INFORMATION:
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Sequence 4, Application US/10336840

Publication No. Us20030219454A1

GENERAL INFORMATION:

APPLICANT: TERRY, TAMSIN DEBORAH

APPLICANT: TERRY, TAMSIN DEBORAH

APPLICANT: DENNINGS, MICHAEL PAUL

APPLICANT: JENNINGS, MICHAEL PAUL

APPLICANT: JENNINGS, MICHAEL PAUL

TITLE OF INVENTION: HARMAGGLUTININ ANTIGEN

FILE REFERENCE: 37955-0007

CURRENT FILING DATE: 2003-01-06

PRIOR APPLICATION NUMBER: PCT/AU01/00822

PRIOR APPLICATION NUMBER: PCT/AU01/00822

PRIOR PLING DATE: 2001-07-06

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin Ver. 2.1

**ERQ ID NO 4**
APPLICANT: TERRY, TAMSIN DEBORAH
APPLICANT: TSENG, HSING-JU
APPLICANT: HOBB, RHONDA IVA
APPLICANT: JENNINGS, MICHAEL PAUL
APPLICANT: JENNINGS, JOHN
TITLE OF INVENTION: HAEMAGGLUTININ ANTIGEN
FILE REFERENCE: 37955-0007
CURRENT APPLICATION NUMBER: US/10/336,840
                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/AU01/00822
PRIOR FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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Best Local Similarity 44.6%;
Matches 152; Conservative 4
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                  18; Gaps
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Best Local Similarity 44.6%; Pred. No. 1.2e-54; Matches 152; Conservative 46; Mismatches 125;
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Search completed: January 19, 2005, 18:31:06 Job time : 531 secs

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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

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3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

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US-08-836-500A-2

US-09-679-750-2

US-09-634-681A-7922

US-08-836-500A-4

US-09-809-665A-151

US-09-418-980-8

US-09-418-980-8

US-09-457-921B-2

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US-09-328-352-5219

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Sequence 13729, A Sequence 13729, A Sequence 13729, A Sequence 29681, A Sequence 13, Appl Sequence 13, Appl Sequence 1373, A Sequence 5621, Ap Sequence 5621, Ap Sequence 6621, Ap Sequence 6, Appli 3190, Ap 4, Appli Sequence Sequence Sequence US-08-572-447C-11 US-09-267-747-11 US-09-252-91A-18046 US-09-252-91A-13729 US-09-328-352-6870 US-09-328-352-6870 US-09-252-991A-29681 US-09-252-991A-29681 US-09-267-777-13 US-09-267-91A-19373 US-09-267-91A-26245 US-09-252-991A-19373 US-09-267-91A-19373 US-09-267-91A-19373 US-09-267-91A-19373 US-09-267-91A-19373 US-09-674-779B-6 US-09-674-779B-6 US-09-674-779B-6 US-09-674-779B-6 1161 2661 2661 2722 2722 2724 2724 2724 2731 2721 2721 2722 2731 272 

## ALIGNMENTS

US-09-489-039A-7451

GENERAL INFORMATION:

APPLICANT:
APPLICANT:
GATY Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REPERBNCE: 2709.2004001
CURRENT APPLICATION NUMBER: US,09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7451 245 106 286 305 287 MDFKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 346 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA 125 STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV 185 226 65 EMGYDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYA SYREGOEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGOOALDOLYTOLSN VAQAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF STGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGV SYRFGGEDAAPVVAPAAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSN MDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVT 6 VLNAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGF Gaps ; 0 Length 385; 2; Indels Score 1782; DB 4; Pred. No. 5e-169; 0; Mismatches 2; GNTCDNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPA Sequence 7451, Application US/09489039A Patent No. 6610836 ORGANISM: Klebsiella pneumoniae 97.8%; Best Local Similarity 99.4 Matches 336, Conservative US-09-489-039A-7451 107 126 167 227 99 186 246 Query Match 306 TYPE: PRT g 음 음 ઠે g ò ⋩ ò ò à

RESULT

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RESULT 3
US-09-679-750-2
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                                                                                      APPLICANT: Binz, Hans
APPLICANT: Baussant, Thierry
APPLICANT: Haeuw, Jean-Francois
APPLICANT: Haeuw, Jean-Francois
APPLICANT: Housen blook in the new trien of the new trien of the new trien of the new trien of the new trien of the new trien of the new trien of the new trien of the new trien of the new trien of the new trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien of trien o
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                                                                                                                                                                                                                                                                               Patent No. 6197929
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.7%; Score 1781; DB 3; I
100.0%; Pred. No. 5.1e-169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/836,500A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
REFRENCE/DOCKET NUMBER: PIEI514P0180US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
   Sequence 2, Application US/08836500A
Patent No. 6197929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 335; Conservative
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MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
                                                             GENERAL INFORMATION: APPLICANT: Binz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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AFFILCENT. Thierry
Baussant, Thierry
Haeuw, Jean-Francois
Nguyen Ngoc, Thien
TITLE OF INVENTION: Carrier Protein Having an Adjuvant
Effect, Immunogenic Complex Containing It, Process f
Their Preparation, Nucleotide Sequence and Vaccines 189 180 249 181 GQEDAAPVVAPAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPK 240 DGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTC 309 DWIGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKGNYASTGV 129 9 GOEDAAPVVABAAPAPAPEVATKHFILKEDVLENFNKATLKPEGQQALDQLYTQLSNMDPK SRSEHDTGVSPVFAGGVENAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYRF SRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYRF 10 APKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEMGY ; 0 97.7%; Score 1781; DB 4; Length 335; 100.0%; Pred. No. 5.1e-169; NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
RADDRESSEE: ADDRESSEE: STREET: 180 N. Stetson, 2 Prudential Plaza, Suite Indels COMPUTER: IBM PC formatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 REFERENCE/DOCKET NUMBER: PIE1514P0180US TELECOMMUNICATION INFORMATION: 100.0%; Pred. No. 5.1 ive 0; Mismatches CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/679,750
FILING DATE: 08-Oct-2000
CLASSIFICATION: <Unknown> APPLICATION NUMBER: 08/836,500 FILING DATE: «Unknown» ATTORNEY/AGENT INFORMATION: TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 2: NAME: Katz, Martin L. REGISTRATION NUMBER: 25,011 MEDIUM TYPE: Floppy disk Sequence 2, Application US/09679750 Patent No. 6780420 GENERAL INFORMATION: TELEPHONE: 312-616-5400 TELEFAX: 312-616-5460 LENGTH: 335 amino acids TYPE: amino acid SEQUENCE CHARACTERISTICS INFORMATION FOR SEQ ID NO: 2 ZIP: 60601 COMPUTER READABLE FORM: PRIOR APPLICATION DATA: APPLICANT: Binz, Hans Query Match
Best Local Similarity 100.
Matches 335; Conservative CITY: Chicago STATE: Illinois COUNTRY: U.S.A.

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APPLICANI: Dime, ......
Baussant. Thierry
Haeuw, Jean-Francois
Nguyen Ngoc, Thien
TITLE OF INVENTION: Carrier Protein Having an Adjuvant
Effect, Immunogenic Complex Containing It, Process for
Their Preparation, Nucleotide Sequence and Vaccines
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NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Rockey, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                      COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PITITAL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
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Pred. No. 5.3e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                       ATTORNEY DATE:
CLASSIPTCATION: 424
ATTORNEY AGENT INFORMATION:
NAME: REAZ, MARTIN L.
REGISTRATION NUMBER: 25,011
REFERENCE/DOCKET NUMBER: 25,011
TELECOMMUNICATION INFORMATION:
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09679750
Patent No. 6780420
GENERAL INFORMATION:
APPLICANT: Binz, Hans
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 179; Conservative
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COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                        ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Chicago
                             Chicago
Illinois
                                                                                           U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-836-500A-4
                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-679-750-4
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APPLICANT: GARY BRETON
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7922
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APPLICANT: Baussant, Thierry
APPLICANT: Haeuw, Jean-Francois
APPLICANT: Nguyen Ngoc, Thien
TITLE OF INVENTION: Carrier Protein Having an Adjuvant
TITLE OF INVENTION: Effect, Immunogenic Complex Containing It, Process for
TITLE OF INVENTION: Their Preparation, Nucleotide Sequence and Vaccines
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241 DGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YDWLGRMAYKGSVDNGAFKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADSKG--NYAS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 TGVSR--SEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSYRFGQEDAAPVVAPAP--APAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQ 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 VAYRFNQETPAPVVEPAPVVAPAPVVENKTFTLRSDVLFNYNKSSLKAEGQEALNGLYNE 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESN 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 AAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQVNPYLGFEMG
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STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 1279; DB 4; 1; Pred. No. 6.7e-119; 32; Mismatches 59;
                                                              310 DNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPAG 344
                                                                                              301 DNVKARAALIDCLAPDRRVEIEVKGYKEVVTQPAG 335
                                                                                                                                                                                                                                                                            Sequence 7922, Application US/09543681A Patent No. 6605709
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Best Local Similarity 71.5%;
Matches 243; Conservative 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Proteus mirabilis
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                     -09-543-681A-7922
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US-08-836-500A-4
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SVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKE 337
YQILNQDKLGLAABLGYDYFGRVRGSEKPNGKADKKTFRHAAHGATIALKPSYEVLPDLD 130
                                                                               218 DVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQ 277
                                                                                                                                                                                                                                                                                           APPLICANT: Campos, Manuel
APPLICANT: Baarsch, Mary Jo
APPLICANT: Rosey. Everatt
APPLICANT: Rosey. Everatt
APPLICANT: Antenbauer. Robert
APPLICANT: Warren-Stewart, Lynn
APPLICANT: Warren-Stewart, Lynn
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APPLICANT: Warren-Stewart
APPLICANT: Warren-Stewart
APPLICANT: POSSEA
FILE REFERENCE: PC9854A
CURRENT FILING DATE: 199-10-14
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 IYTRIG-GMVWRADSKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNN
                                                                                                                                       166 IGDA-----GTVGTRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPAFTKHFTLKS
                                                                                                                                                              57 YOV -- NPYLGF -- EMGYDWLGRM -- -- AYKGSVDNGAFK -- AQGVQLTAKLGYPITDDLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 IYTRLG-GMVWRADSKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , ORGANISM: Actinobacillus pleuropneumoniae US-09-418-980-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 8, Application US/09418980
; Patent No. 6713071
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               362 V 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 151, Application US/09809665A

Patent No. 679050
GENERAL INFORMATION:
APPLICANT: Lowery E., David, et al.
TILE OF INVENTION: Anti-Bacterial Vaccine Compositions
FILE REFERENCE: 28341/00435
CURRENT APPLICATION NUMBER: US/09/809,665A
CURRENT APPLICATION NUMBER: 60/153,453
PRIOR FILING DATE: 2001-03-15
PRIOR PRIOR FILING DATE: 1999-04-09
PRIOR PRILING DATE: 1999-04-09
PRIOR PRILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 197
SOFFWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                          NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
REFERENCE/DOCKET NUMBER: PIE1514P0180US
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
54.0%; Score 984; DB 4;
Best Local Similarity 100.0%; Pred. No. 5.3e-90;
Matches 179; Conservative 0; Mismatches 0;
                      APPLICATION NUMBER: US/09/679,750 FILING DATE: 08-Oct-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Actinobacillus pleuropneumoniae
US-09-809-665A-151
                                                                             PRIOR APPLICATION DATA:

APPLICATION WUBER: 08/836,500
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-679-750-4
                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: amino acid
    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-809-665A-151
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Best Local Si
Matches 153
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241 277

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57 YOV----GVQLTAKLGFEMGYDWLGRMAYKGSVDNGAFKAQ----GVQLTAKLGYPITDDLDIY 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 IG-----DAGTVGTRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPAPAFTKHFTLKSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.3%; Score 662.5; DB 3; Length 359; 43.3%; Pred. No. 1.7e-57;
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                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A>
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/467,722A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49; Mismatches 121;
                                                                                                                                                                                   AUDRESSEE: Calfee, Halter and Griswold STREET: Suite 1800 800 Superior Avenue CITY: Cleveland STATE: Ohio
                                                                                      Sequence 2, Application US/08467722A
Patent No. 6030626
GENERAL INFORMATION:
APPLICANT: KOLATURUDY, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22727/00102
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLITICK, Mary E.
REGISTATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 2272
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                           US-08-467-722A-2
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US-09-451-184-2
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57 YQV----NPYLGFEMGYDWLGRMAYKGSVDNGAPKAQ----GVQLTAKLGYPITDDLDIY 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
PLEATION NUMBER: US/08/457,997B
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 662.5; DB 1;
; Pred. No. 1.7e-57;
49; Mismatches 121;
                                                                                                                                                                          Sequence 2, Application US/08457997B
Patent No. 5766608
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kolattukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   ADDRESSEE: Calfee, Halter and Griswold STREET: Suite 1800 800 Superior Avenue CITY: Cleveland STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22727/00102
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCORNEY/AGENT INFORMATION:
NAME: GOLTICK, Mary E.
REGISTRATION NUMBER: 34,829
REFRENCE/DOCKET NUMBER: 2272
TELEPHONE: (216) 622-8458
TELEPHONE: (216) 622-8458
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.3%;
43.3%;
                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 36.39
Best Local Similarity 43.33
Matches 155; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
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                                                   338 V 338
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Gaps

33;

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; TITLE OF INVENTION: Anti-Bacterial Vaccine Compositions
FILE REPERENCE: 28341/00435
; CURRENT APPLICATION NUMBER: US/9/809,665A
; CURRENT PLING DATE: 2001-03-15
; PRIOR FILING DATE: 1999-09-10
; PRIOR PLING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/128,689
PRIOR PLING DATE: 1999-04-09
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 153
LENGTH: 369
                                                                                                                                                                                                                                                                                                                                                                              Query Match 35.5%; Score 646.5; DB 4; Best Local Similarity 41.1%; Pred. No. 6.9e-56; Matches 153; Conservative 60; Mismatches 110;
                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Actinobacillus pleuropneumoniae
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356 RVEVQVQGAKNV 367
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                                                                                                                                                                                                                                                                                                                                       US-09-809-665A-153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 TRLGGMVWRADSKGNYASTGV---SRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNN 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 IG-----DAGTVGTRPDNGMLSLGVSYRFGQEDAAPVVAPAPAPAPEVATKHFTLKSD 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 VLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLSEKRAQS 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 VVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYK 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 LAAASVAQAAPQENTFYAGVKAGQGSFHDGINNNGAIKKGLSSSNYGYRRNTFTYGVFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHD----TGFYGNGFQNNNGPTRNDQLGAGAFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.3%; Score 662.5; DB 4; Length 359;
43.3%; Pred. No. 1.7e-57;
tive 49; Mismatches 121; Indels 33
                                                                                                                                                                                                                                              COUPTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/451,184
                                                             APPLICANT: Kolatukudy, P. E.
TITLE OF INVENTION: Otitis Media Vaccine
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
STREET: 1400 McDonald Investment Center,
STREET: 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Docherty, Pamela A.
REGISTRATION NUMBER: 40,591
REFERENCE/DOCKET NUMBER: 24547/04000
TELECOMMUNICATION INFORMATION:
TELEPAX: (216) 622-8416
TELEPAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
Sequence 2, Application US/09451184 Patent No. 6562349 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 359 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 43.3
Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-09-451-184-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
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Sequence 153, Application US/09809665A Patent No. 6790950 GENERAL INFORMATION: APPLICANT: Lowery E., David, et al.

RESULT 12 US-09-809-665A-153

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APPLICANT: Campos, Manuel
APPLICANT: Campos, Mary Jo
APPLICANT: Baarsch, Mary Jo
APPLICANT: Ankenbauer, Robert
APPLICANT: Ankenbauer, Lynn
APPLICANT: Warren-Stewart, Lynn
APPLICANT: Warren-Stewart, Lynn
APPLICANT: Warren-Stewart, Lynn
APPLICANT: Keach, Robin
ITILE OF INVENTION: NOVEL PROTEINS FROM ACTINOBACILLUS PLEUROPNEUMONIAE
FILE REFERENCE: PC9884A
CURRENT APPLICATION NUMBER: US/09/418,980
CURRENT FILING DATE: 1999-10-14
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 369
                                                                                                                                                                                                                                                   67 TYGVFGGYQILNQNNFGLAABLGYDYYGRV--RGNVDE--FRTVKHSAHGLNLALKPSYE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 GAGAFGGYQV----NPYLGFEMGYDWLGRMAYKGSVDNGAFK-----AQGVQLTAKLGYP 100
                                                                                                                                                                                                                                                                                                                              101 ITDDLDIYTRLGGMVWRADSKGNYASTGVSRSE---HDTGVSPVFAGGVEWAVTRDIATR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                          158 LEYQWVNNIGDAGTV----GTR-----PDNGMLSLGVSYRFGQEDAAPVVAPAPAPAP 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 EVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 YNQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDR 326
                                                                                                                                      Gaps
Length 369;
                                                                                                          1 MKAIFVLNAAPKDNTWYAGGKLGWSQYHDTGFYG-NGFQNNNGPTRNDQ-
                                                      Indels
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APPLICANT: Binz, Hans
APPLICANT: Baussant, Thierry
APPLICANT: Haeuw, Jean-Francois
APPLICANT: Haeuw, Jean-Francois
APPLICANT: Haeuw, Jean-Francois
TITLE OF INVENTION: Carrier Protein Having an Adjuvant
TITLE OF INVENTION: Effect, Immunogenic Complex Containing It, Process for TITLE OF INVENTION: Their Preparation, Nucleotide Sequence and Vaccines
                                                                                                                                                                                                               57 YQV----NPYLGFEMGYDWLGRMAYKGSVDNGAFKAQ----GVQLTAKLGYPITDDLDIY 108
                                                                                                                                                                                                                                       109 TRLGGMVWRADSKGNYASTGV---SRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNN 165
                                                                                                                                                                                                                                                                                                               IG-----DAGTVGTRPDN-----GMLSLGVSYRFGQEDAAPVVAPAPAPAPEVATKH 212
                                                                                                                                                                                                                                                                                                                                                                                            217 FSLINLDVTFAFGKANLKPQAQATLDSIYGEMSQV--KSAKVAVAGYTDRIGSDAFNVKLS 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAFGG 56
                                                                                                                                                        FTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYNQQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRRVEIEV
                                                                                              Gaps
                                                                                              63;
                                                          Length 338;
                                                                                                                                    10 APKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson, 2 Prudential Plaza, Suite
STREET: 4700
STREET: Chicago
STATE: 11linois
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,500A
                                                        32.2%; Score 586.5; DB 1;
40.1%; Pred. No. 5.8e-50;
trive 44; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIE1514P0180US
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08836500A Patent No. 6197929 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Katz, Martin L.
                                                                                              Matches 146; Conservative
  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6197929
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, M
                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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US-08-836-500A-6
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US-08-210-394-1
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                                                          Query Match
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VENTION: Purified No. 5770213typable Haemophilus
VENTION: influenzae P5 Protein as a Vaccine for No. 5770213typable
VENTION: Haemophilus Influenzae Strain
                                                                              11;
                                                                                                                                                                                                                                                                 101 ITDDLDIYTRLGGMVWRADSKGNYASTGVSRSE--HDTGVSPVFAGGVEWAVTRDIATRL 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NQQLSEKRAQSVVDYLVAKGIPAGKISARGMGESNPVTGNTCDNVKARAALIDCLAPDRR 327
                                                                                                                                      67 TYGVFGGYQILMQNNFGLATELGYDYYGRV--RG--NDGEFRAMKHSAHGLNFALKPSYE
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                                                                              Gaps
                                                                            47;
                                        Length 369;
                                    35.1%; Score 639.5; DB 4; Length 340.7%; Pred. No. 3.4e-55; ive 60; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/210,394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ольк: US/08/210,394
07-MAR-1994
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Patent No. 5770213
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Harrington, James J
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201/831-3246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                          Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SS: unknown unknown
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zlotnick
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Wayne
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: unk
                                    Query Match
Best Local Similarity
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STREET: One
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US-09-418-980-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-08-210-394-1
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117 RADSKGNYASTGVSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRP 176
                                                                                                                                                                                                    0; Gaps
                                                                                                                                                              Query Match 20.8%; Score 379; DB 3; Length 72; Best Local Similarity 100.0%; Pred. No. 2.7e-30; Matches 72; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                         Search completed: January 19, 2005, 18:17:29
Job time : 26 secs
                      ;
TELEFAX: 312-616-5460;
INFORMATION POR SEO ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 amino acids
TYPE: amino acids
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: protein
US-08-936-500A-6
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61 DNGMLSLGVSYR 72
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